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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:12:47 ; Search time 23 Seconds

(without alignments)  
710.508 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRLGIMKRSSV 394

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	1	CIW3_HUMAN
2	1850.5	90.6	411	1	CIW3_RAT
3	1840.5	90.1	409	1	CIW3_MOUSE
4	1116	54.7	374	1	CIW9_HUMAN
5	1069.5	52.4	365	1	CIW9_CAVPO
6	370	18.1	411	1	CIW2_MOUSE
7	364	17.8	426	1	CIW2_MOUSE
8	349.5	17.1	538	1	CIW2_MOUSE
9	349.5	17.1	538	1	CIW2_MOUSE
10	329.5	16.1	393	1	CIW4_HUMAN
11	326.5	16.0	398	1	CIW4_MOUSE
12	320.5	15.7	336	1	CIW1_HUMAN
13	319	15.6	499	1	CIW5_MOUSE
14	318.5	15.6	336	1	CIW1_MOUSE
15	295.5	14.5	313	1	CIW6_HUMAN
16	261.5	12.8	1001	1	ORL1_MOUSE
17	259.5	12.7	335	1	TKR8_CAEEL
18	224	11.0	307	1	CIW7_HUMAN
19	221	10.8	307	1	CIW8_MOUSE
20	170	8.3	691	1	TKR1_YEAST
21	112.5	5.5	490	1	CIW1_MOUSE
22	100	4.9	694	1	CIW2_MOUSE
23	99.5	4.9	1174	1	CIW2_MOUSE
24	98	4.8	1743	1	TKR1_MOUSE
25	97.5	4.8	228	1	TKR1_MOUSE
26	97.5	4.8	432	1	TKR1_MOUSE
27	96.5	4.7	449	1	TKR1_MOUSE
28	94.5	4.6	209	1	TKR1_MOUSE
29	94.5	4.6	385	1	TKR1_MOUSE
30	94.5	4.6	449	1	TKR1_MOUSE
31	94.5	4.6	647	1	TKR1_MOUSE
32	94	4.6	262	1	TKR1_MOUSE
33	94	4.6	287	1	TKR1_MOUSE

34	94	4.6	1159	1	HERG_HUMAN
35	93.5	4.6	285	1	WZC2_ARATH
36	93	4.6	529	1	CIW6_HUMAN
37	93	4.6	602	1	CIW5_RAT
38	92.5	4.5	565	1	DSBD_ECO57
39	92.5	4.5	653	1	CIW4_HUMAN
40	92.5	4.5	655	1	CIW4_RAT
41	92.5	4.5	685	1	FZD8_MOUSE
42	92	4.5	451	1	IFR1_HUMAN
43	92	4.5	598	1	CIW5_RABIT
44	91.5	4.5	660	1	CIW4_BOVIN
45	91.5	4.5	1581	1	VGLP_BEV

## ALIGNMENTS

RESULT 1	ID	CIW3_HUMAN	STANDARD:	PRT:	394 AA.
AC	014649				
DT	16-OCT-2001 (rel. 40, Created)				
DT	16-OCT-2001 (rel. 40, Last sequence update)				
DT	15-JUN-2002 (rel. 41, Last annotation update)				
DE	Potassium channel subfamily K member 3 (acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).				
GN	KCNK3 OR TASK.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.				
OX	NCBI_Taxid-9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE-97459932; PubMed-9312005;				
RA	Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;				
RT	"TASK, a human background K+ channel to sense external pH variations near physiological pH."				
RT	near physiological pH."				
RL	EMBO J. 16:5464-5471(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Heart;				
RA	Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,				
RT	Goldstein S.A.N.;				
RT	"Proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3."				
RT	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	ACTIVATION.				
RX	MEDLINE-99254548; PubMed-10321245;				
RA	Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;				
RT	"Inhalational anesthetics activate two-pore-domain background K+ channels."				
RT	Nat. Neurosci. 2:422-426(1999).				
CC	- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE. BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein (potensial).				
CC	- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.				
CC	- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY HALOTHANE AND ISOFLURANE.				
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.				
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CC -----

DR EMBL: AF006823; AAC5177.1; -

DR EMBL: AF065163; AAC29340.1; -

DR Genew; HGNC:6278; KCNK3.

DR MIM; 603220; -

DR InterPro: IPR003280; K+channel\_2pore.

DR InterPro: IPR001622; K+channel\_pore.

DR InterPro: IPR000636; M+channel\_nlg.

DR InterPro: IPR003092; TASK\_channel.

DR Pfam; PF00520; Ion\_trans.1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KM Glycoprotein.

FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 9 29 POTENTIAL.

FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).

FT TRANSSEM 108 128 POTENTIAL.

FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 159 179 POTENTIAL.

FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

FT TRANSSEM 223 243 POTENTIAL.

FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).

SO SEQUENCE 394 AA; 43518 MW; 9FAC8266F615F87 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;

Best Local Similarity 100.0%; Pred. No. 1e-153;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVTTALIVCTFTYLLVGAADFDALESEBELIERORLELROQLRARVNLSCGYE 60

DB 1 MKRONVTTALIVCTFTYLLVGAADFDALESEBELIERORLELROQLRARVNLSCGYE 60

QY 61 ELERVVLRKPKHAGVQWRAGSFYATVYTTIGGHAAPSTDGKVCMEFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRAGSFYATVYTTIGGHAAPSTDGKVCMEFYALLGIP 120

QY 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANWLVGFSCISITLCIGAAAFSH 180

DB 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANWLVGFSCISITLCIGAAAFSH 180

QY 181 YEHMTFFQAYVYCFITLTITGFDYVALOKDQALQTOPQVAVSFYILTLGTVIGAF 240

DB 181 YEHMTFFQAYVYCFITLTITGFDYVALOKDQALQTOPQVAVSFYILTLGTVIGAF 240

QY 241 LVVLRPTMNAEDEKRDARHALLTRNGAGGGGSAHTTDTASTAAGGGGFRNVY 300

DB 241 LVVLRPTMNAEDEKRDARHALLTRNGAGGGGSAHTTDTASTAAGGGGFRNVY 300

QY 301 AEVLHFOSMSCLMYRSREKLOYSTIPMIIPRODSTPCVQSHSSGGGGRYSDPSSR 360

DB 301 AEVLHFOSMSCLMYRSREKLOYSTIPMIIPRODSTPCVQSHSSGGGGRYSDPSSR 360

QY 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2

CIW3\_RAT

AC 054912; STANDARD; PRT; 411 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).

GN KCNK3 OR TASK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cerebellum;

RX MEDLINE=98099797; Pubmed=9437008;

RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsaeth J.R., Yost C.S.;

RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum".

RL J. Neurosci. 18:868-877(1998).

CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART, MODERATE EXPRESSION IN LUNG AND BRAIN, LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.

CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPRYACINE AND PHENTOLIN. ACTIVATED BY PROTEIN KINASE A.

CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

CC -----

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CC -----

DR EMBL: AF031384; AAC39952.1; -

DR InterPro: IPR003280; K+channel\_2pore.

DR InterPro: IPR001622; K+channel\_pore.

DR InterPro: IPR000636; M+channel\_nlg.

DR InterPro: IPR003092; TASK\_channel.

DR Pfam; PF00520; Ion\_trans.1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KM Glycoprotein.

FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 9 29 POTENTIAL.

FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).

FT TRANSSEM 108 128 POTENTIAL.

FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 159 179 POTENTIAL.

FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

FT TRANSSEM 223 243 POTENTIAL.

FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).

SO SEQUENCE 411 AA; 45276 MW; D2778016E09E2B5 CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;

Best Local Similarity 88.3%; Pred. No. 1.3e-138;

Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;

QY 1 MKRONVTTALIVCTFTYLLVGAADFDALESEBELIERORLELROQLRARVNLSCGYE 60

DB 1 MKRONVTTALIVCTFTYLLVGAADFDALESEBELIERORLELROQLRARVNLSCGYE 60

QY 61 ELERVVLRKPKHAGVQWRAGSFYATVYTTIGGHAAPSTDGKVCMEFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRAGSFYATVYTTIGGHAAPSTDGKVCMEFYALLGIP 120

QY 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANWLVGFSCISITLCIGAAAFSH 180

DB 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANWLVGFSCISITLCIGAAAFSH 180

QY 181 YEHMTFFQAYVYCFITLTITGFDYVALOKDQALQTOPQVAVSFYILTLGTVIGAF 240

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Db 181 YEHMTFQAYYYCFTLTITGFDVVALQKQDALOTQPOYVAFSFTVLTGLTVGAPLN 240
Qy 241 LVLRFTMTMNADEKRDRAEHALLTRNGQAGCGG-----GGSATTTDTASTAA- 291
Db 241 LVLRFTMTMNADEKRDRAEHALLTRNGQAGCGGSLSDGVPRPRPYCAAAAG 300
Qy 292 -----GGGFRNVAEVLHFOQSMCCLMYKSKREKQYSIPMIIPRDLSTSDTCVROS 343
Db 301 GGVGVGVGGSGFRNVAEVLHFOQSMCCLMYKSKREKQYSIPMIIPRDLSTSDTCVROS 360
Qy 344 HSPGGGGGRYSDTPSRRCISGAPRSATSSVTGSHSLSTFRGLMKRRSSV 394
Db 361 HSPGGGGGRYSDTPSRRCISGAPRSATSSVTGSHSLSTFRGLMKRRSSV 411

RESULT 3
CITW3_MOUSE STANDARD; PRT: 409 AA.
AC 035111; 035163;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE channel protein TASK) (TWIK-related acid-sensitive K+ channel).
DE {Cardiac two-pore background K+ channel} (CTBAK-1).
GN KCNK3 OR TASK OR CTBAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RA MEDLINE=9616556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurachi Y.;
RA "Cloning and functional expression of a novel cardiac two-pore
RA background K+ channel (CTBAK-1).";
RA Circ. Res. 82:513-518(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RA MEDLINE=20287574; PubMed=10748056;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RA "Proton block and voltage gating are potassium-dependent in the
RA cardiac leak channel KCNK3";
RA J. Biol. Chem. 275:16969-16978(2000).
RN [3]
RP SEQUENCE OF 4-409 FROM N.A.
RA MEDLINE=97459932; PubMed=9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RA "TASK, a human background K+ channel to sense external pH variations
RA near physiological pH.";
RA Embo J. 16:5464-5471(1997).
RN [4]
RP FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
RN CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
RN ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
RN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW
RN WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
RN (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
CC INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
CC DR EMBL; AB008537; BAA25436.1; -
CC DR EMBL; AF241798; AAF81418.1; -
CC DR EMBL; AF242508; AAF81418.1; JOINED.
CC DR EMBL; AF065162; AAG29339.1; -
CC DR EMBL; AF006824; AAC53367.1; -
CC DR EMBL; AB013345; BAA28349.1; -
CC DR MGI; MGI:1100509; Kcnk3.
CC DR InterPro: IPR003280; K+channel_2pore.
CC DR InterPro: IPR001622; K+channel_pore.
CC DR InterPro: IPR000636; K+channel_nlg.
CC DR InterPro: IPR003092; TASK_channel.
CC DR Pfam; PF00520; Ion_Trans_1.
CC DR PRINTS; PR01333; 2PORECHANNEL.
CC DR PRINTS; PR01095; TASKCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
CC FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 9 29 POTENTIAL.
CC FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
CC FT TRANSMEM 108 128 POTENTIAL.
CC FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 159 179 POTENTIAL.
CC FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
CC FT TRANSMEM 223 243 POTENTIAL.
CC FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 4 4 Q -> E (IN REF. 3).
CC FT CONFLICT 123 123 V -> I (IN REF. 3).
CC SQ SEQUENCE 409 AA; 45068 MW; 352368011AAC5687 CRC64;

Query Match 90.1%; Score 1840.5; DB 1; Length 409;
Best Local Similarity 88.5%; Pred. No. 8.1e-138;
Matches 362; Conservative 7; Mismatches 25; Indels 15; Gaps 2;

Qy 1 MKRONVRLALIVCFITLLVGAIVFDLSEPELEIQRLELRQELRARNLSQGYE 60
Db 1 MKRONVRLALIVCFITLLVGAIVFDLSEPELEIQRLELRQELRARNLSQGYE 60
Qy 61 ELERVYLRKPKKAGVORFAGSFYATVYTTIGYGAAPSTDGKVFCEYALLGTP 120
Db 61 ELERVYLRKPKKAGVORFAGSFYATVYTTIGYGAAPSTDGKVFCEYALLGTP 120
Qy 121 TLVVFQSLGERINTLVRYLLHRAKKGICMRADVSMANVLLGFESCISTLCIGAAFSH 180
Db 121 TLVVFQSLGERINTLVRYLLHRAKKGICMRADVSMANVLLGFESCISTLCIGAAFSH 180
Qy 181 YEHMTFQAYYYCFTLTITGFDVVALQKQDALOTQPOYVAFSFTVLTGLTVGAPLN 240
Db 181 YEHMTFQAYYYCFTLTITGFDVVALQKQDALOTQPOYVAFSFTVLTGLTVGAPLN 240
Qy 241 LVLRFTMTMNADEKRDRAEHALLTRNGQAGCGG-----GGSATTTDTASTAA- 291
Db 241 LVLRFTMTMNADEKRDRAEHALLTRNGQAGCGGSLSDGVPRPRPYCAAAAG 300
Qy 292 -----GGGFRNVAEVLHFOQSMCCLMYKSKREKQYSIPMIIPRDLSTSDTCVROS 343
Db 292 -----GGGFRNVAEVLHFOQSMCCLMYKSKREKQYSIPMIIPRDLSTSDTCVROS 360
Qy 344 HSPGGGGGRYSDTPSRRCISGAPRSATSSVTGSHSLSTFRGLMKRRSSV 394
Db 344 HSPGGGGGRYSDTPSRRCISGAPRSATSSVTGSHSLSTFRGLMKRRSSV 409

RESULT 4
CITW9_HUMAN STANDARD; PRT: 374 AA.
AC 09NFC2;
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Potassium channel subfamily K member 9 (Acid-sensitive potassium  
 DE channel protein TASK-3) (TWIK-related acid-sensitive K<sup>+</sup> channel 3).  
 GN KCNK9 OR TASK3.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20287530; PubMed-10747866;  
 RA Rajan S., Wismeyer E., Liu G.X., Preisig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RT J. Biol. Chem. 275:16650-16657(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Cerebellum;  
 RX MEDLINE-2049203; PubMed-11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
 RA Kelsall R.E., Muddock P.R., Randall A.D., Rennie G.I., Gloger I.S.;  
 RT "Cloning, localization and functional expression of a novel human,  
 RT cerebellum specific, two pore domain potassium channel.";  
 RT Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Girard C., Lesage F., Tinel N., Lazdunski M.;  
 RT "Human Task-3, a novel 2p domain potassium channel related to Task.";  
 RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,  
 RA Coetzee W., Rudy B.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF212829; AAF63708.1; -;  
 DR EMBL: AF248241; AAG31730.1; -;  
 DR EMBL: AF279809; AAF85982.1; -;  
 DR EMBL: AF257080; AAG33126.1; -;  
 DR Gene: HGNC:6283; KCNK9.  
 DR MIM: 605874; -;  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PRO133; 2PORKCHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KM Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 219 239 POTENTIAL.

FT DOMAIN 240 374 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 374 AA; 42263 MM; 8A19AEFE5A4D7E38 CRC64;  
 Query Match 54.78; Score 1116; DB 1; Length 374;  
 Best Local Similarity 59.08; Pred. No. 8.7e-81;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
 OY 1 MKRONRTALIVCTFYLLVGAADVDALESEBELERORLELROGLRARYLSOGGE 60  
 DB 1 MKRONRTSLIVCTFYLLVGAADVDALESEBELERORLELROGLRARYLSOGGE 60  
 OY 61 ELERVYLRKPKRAGVQWRPAGSFPAITVITTYIGYGAHPSTGGKVCMPYALGIP 120  
 DB 61 QELVILQSEPHRAGVQWRPAGSFPAITVITTYIGYGAHPSTGGKVCMPYALGIP 120  
 OY 121 TLVMPQSLGERITVLYLLHRRKKLRADYVSNANVLYGFECISTLCGAAPFSH 180  
 DB 121 TLVMPQSLGERITVLYLLHRRKKLRADYVSNANVLYGFECISTLCGAAPFSH 180  
 OY 181 YEHMTEFOAYVYCFITLTTIGFDVYALQKDALQPOVAFSFIYITGLTVIGAFIN 240  
 DB 181 CEEMSFPHAYVYCFITLTTIGFDVYALQKDALQKPLVAFSFIYITGLTVIGAFIN 240  
 OY 241 LVVLRFTVNADEKRDARHALLFRNGAGGGGCGSAHTDTASTAAAGCGGRNVY 300  
 DB 241 LVVLRFTVNADEKRDARHALLFRNGAGGGGCGSAHTDTASTAAAGCGGRNVY 300  
 OY 301 -NEVLHFOGSCGLWKKREKQYISPMIIPRLSTSDVCESHSPPGGGRYSPTR 359  
 DB 287 KADVPDQSCVCTCRSDQ---YGRSVAPONSFAKLAPHYFHSYKIEIETSTUK 343  
 OY 360 RCICSGAPRSATSVSTGLHSLSTFGMLKRRSSV 394  
 DB 344 NSLFP---SPISISIPGLHSFIDHQRLLMKRRRSV 374  
 RESULT 5  
 C1M9\_CAVPO  
 ID C1M9\_CAVPO STANDARD; PRT; 365 AA.  
 AC 09UL58;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DE Potassium channel subfamily K member 9 (acid-sensitive potassium  
 DE channel protein TASK-3) (TWIK-related acid-sensitive K<sup>+</sup> channel 3).  
 GN KCNK9 OR TASK3.  
 OS Cavia porcellus (guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-20287530; PubMed-10747866;  
 RA Rajan S., Wismeyer E., Liu G.X., Preisig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RT J. Biol. Chem. 275:16650-16657(2000).  
 RL -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

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CC EMBL: AF212827; AAF63706.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 108 128 POTENTIAL.
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 219 239 POTENTIAL.
FT DOMAIN 240 365 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 365 AA; 40769 MW; 261DC973EF53AF91 CRC64;

Query Match 52.4%; Score 1069.5; DB 1; Length 365;
Best Local Similarity 57.1%; Pred. No. 3.9e-77;
Matches 226; Conservative 43; Mismatches 94; Indels 33; Gaps 6;

OY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROOELRARNYNSGGYE 60
DB 1 MKONVRLSLIACFTYLLVGAAVFDALSDHEKREKEKAEIRIRKYNISTEDYR 60
OY 61 ELERVYLRKPKHKAQVOMRFAQSFYATVTITIGYHAAPSTOGKFCMFYALGIP 120
DB 61 QLEVLIIQSEHRAQVOMKFAQSFYATVTITIGYHAAPSTOGKFCMFYALGIP 120
OY 121 TLVFMQSLGERINTLVRYLHRAKGLRRADYSAMMYLVIGFSCSTLCIGAAAFSH 180
DB 121 TLVFMQSLGERINTLVRYLHRAKGLRRADYSAMMYLVIGFSCSTLCIGAAAFSH 180
OY 121 TLVFMQSLGERINTLVRYLHRAKGLRRADYSAMMYLVIGFSCSTLCIGAAAFSH 180
DB 121 TLVFMQSLGERINTLVRYLHRAKGLRRADYSAMMYLVIGFSCSTLCIGAAAFSH 180
OY 181 YEHTFPQAYYYCFTLTITIGFYDVALQKDALOTQYVAFSVVYLLTGIVYGAFLN 240
DB 181 CEESFFHAYVCFTLTITIGFYDVALQKDALOTQYVAFSVVYLLTGIVYGAFLN 240
OY 241 LVVLRFTMADEKRADEHRAALLTRNGACGGGGGSAHWTDRASSTA--AGCGGFRN 298
DB 241 LVVLRFTMADEKRADEHRAALLTRNGACGGGGGSAHWTDRASSTA--AGCGGFRN 298
OY 241 LVVLRFTMADEKRADEHRAALLTRNGACGGGGGSAHWTDRASSTA--AGCGGFRN 298
DB 241 LVVLRFTMADEKRADEHRAALLTRNGACGGGGGSAHWTDRASSTA--AGCGGFRN 298
OY 299 VYAEVLHFQSMCCLWYKSRKELQYSLPMLIPRDLSTSDTCVEQSHSSPGGGGRYSDPS 358
DB 299 VYAEVLHFQSMCCLWYKSRKELQYSLPMLIPRDLSTSDTCVEQSHSSPGGGGRYSDPS 358
OY 292 -----DLQSVSCACYSRSP--QNFQATLAPQPLHSISCRLEI-----SPS 331
DB 292 -----DLQSVSCACYSRSP--QNFQATLAPQPLHSISCRLEI-----SPS 331
OY 359 RRCLOSGAPRAISSVSGHLSLSTRGLMKRRSSV 394
DB 359 RRCLOSGAPRAISSVSGHLSLSTRGLMKRRSSV 394
OY 332 --TLKNSLFPSPISVSGHLSLSTRGLMKRRSSV 365
DB 332 --TLKNSLFPSPISVSGHLSLSTRGLMKRRSSV 365

RESULT 6
C1W2_MOUSE STANDARD: PRT. 411 AA.
AC P97438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
channel protein TREK-1) (two-pore potassium channel 1PKC1) (TREK-1 K+
channel subunit).
DE KCKN2.
GN KCKN2.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

```

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RC TISSUE-Brain;
RX MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RT uncoupled, outward-rectifier K+ channel.";
RL EMBL J. 15:6854-6862(1996);
RM [2]
RN REVIEWS.
RP TISSUE-Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RP [3]
RX ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC or send an email to license@isb-sib.ch).
CC EMBL: U73488; AAC53005.2; -.
DR MGD: MGI:109366; Kcnk2.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003976; trek_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EPA05 CRC64;

Query Match 18.1%; Score 370; DB 1; Length 411;
Best Local Similarity 28.0%; Pred. No. 5.8e-22;
Matches 109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;

OY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROOELRARNYNSGGYE 60

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Db 42 MKKRTVSTFLVY--VLYLIGAAVFALEQPOEISQRTTIVIOKOTFLAOSHACVNS--T 97
OY 61 ELERVVLR-L-KPKKAGV-----QMRFGSPYPAITVTTTGGYHAAPSTGGKV 108
Db 98 ELDELQOIVAAINAGIIFPLGNSSNOVSHMDLSSFFFGVITTTGGFNGISPRTEGKX 157
OY 109 FCMFVALLGIPPLVLFVFOISGERINTLVRYLLHRAKKGIGMRAD-----VSM 156
Db 158 FCIIVALLGIPLEGLFLLAGVGDLGITF-----GKGIKAVEDTFLKMNVSQKIRI 208
OY 157 ANKVLIGFSCISTLCIGAAASHYHMTFFQAYVYCFITLTITGGDYVALOKDALOT 216
Db 209 ISTIIFILFGCVLFVLPVIFKHIGWSALDAIYFVITLTITGGDYVAGGSD--IEY 266
OY 217 QPOYVAFSVYILITGLTVIGAFNLVY--VLRFMTNAEDEKRDRAHRAALLTRNGAGGGG 274
Db 267 LDFYKPVVFWFLLVGLAYFAVLSMIGDMLRVISKTKTEV-----307
OY 275 GGGSAHTTDTASTAAAGGGGFERNVYAEVLHFSQMSCLWYKSREKLOYSPMIPRDS 334
Db 308 GEFRAHAAEWTA-----NYTAE-----FKETRRLLSVEL-----YDKF 340
OY 335 TSDTCVGEQSHSSPFGGGRYS-D--TPSRCL 362
Db 341 QRATSVKRLISALAGNHNQELTPCRRTL 369

RESULT 7
C1W2_HUMAN STANDARD; PRT; 426 AA.
ID AC 095069; 09HNE3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
DE channel protein TREK-1) (TREK-1 K+ channel subunit) (two-pore
DE potassium channel protein PKC1).
DE KCNK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels."
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANESTHETICS SUCH AS
CC CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC -----
DR EMBL: AF129399; AAD47569.1; -
DR EMBL: AF004711; AAD01203.1; -

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DR Genew; HGNC:6277; KCNK2.
DR MIM; 603219; -.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003976; Trek_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
DR Tonic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 62 82 POTENTIAL.
FT DOMAIN 144 170 PORE-FORMING 1 (POTENTIAL).
FT TRANSEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 224 243 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING 2 (POTENTIAL).
FT TRANSEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT DOMAIN SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
FT TRANSEM SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match 17.8%; Score 364; DB 1; Length 426;
Best Local Similarity 30.6%; Pred. No. 1,8e-21;
Matches 90; Conservative 61; Mismatches 101; Indels 42; Gaps 9;

OY 1 MKRONVRLALVCTFTYLLVGAVALDAESEPELIERORLEQOELRARNVLSGGYE 60
Db 57 MKKRTVSTFLVY--VLYLIGATVFALEQPOEISQRTTIVIOKOTFLSOSHACVNS--T 112
OY 61 ELERVVLR-L-KPKKAGV-----QMRFGSPYPAITVTTTGGYHAAPSTGGKV 108
Db 113 ELDELQOIVAAINAGIIFPLGNSSNOVSHMDLSSFFFGVITTTGGFNGISPRTEGKX 172
OY 109 FCMFVALLGIPPLVLFVFOISGERINTLVRYLLHRAKKGIGMRAD-----VSM 156
Db 173 FCIIVALLGIPLEGLFLLAGVGDLGITF-----GKGIKAVEDTFLKMNVSQKIRI 223
OY 157 ANKVLIGFSCISTLCIGAAASHYHMTFFQAYVYCFITLTITGGDYVALOKDALOT 216
Db 224 ISTIIFILFGCVLFVLPVIFKHIGWSALDAIYFVITLTITGGDYVAGGSD--IEY 281
OY 217 QPOYVAFSVYILITGLTVIGAFNLVY--VLRFMTNAEDEKRDRAHRAALLTRPN 267
Db 282 LDFYKPVVFWFLLVGLAYFAVLSMIGDMLRVISKTKTEVGEFRAHAAEWTA 335

RESULT 8
C1W2_HUMAN STANDARD; PRT; 538 AA.
ID AC P57789; 09HBS9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
DE channel protein TREK-2) (TREK-2 K+ channel subunit).
DE KCNK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RA MEDLINE-20435789; PubMed-10880510;  
 RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;  
 RT "Human TREK2, a 2P domain mechano-sensitive K<sup>+</sup> channel with multiple  
 RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,  
 RT J. Biol. Chem. 275:28398-28405(2000)."  
 RL J. Biol. Chem. 275:28398-28405(2000).  
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY  
 CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.  
 CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING  
 CC UNSATURATED FREE FATTY ACIDS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY  
 CC AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF279890; AAC15191.1; -  
 DR Genbank: HGNC:6273; KCNK10.  
 DR MIM: 605873; -  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 182 202 POTENTIAL.  
 FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 234 254 POTENTIAL.  
 FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 299 319 POTENTIAL.  
 FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 538 AA; 59764 MW; 8E615B08D147FBC CRC64;  
 Query Match 17.1%; Score 349.5; DB 1; Length 538;  
 Best Local Similarity 32.8%; Pred. No. 3.2e-20;  
 Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;

QY 1 MKRONVRLALIVCTFTYLLVGAVFDALESEPELIERORLELROOE-LRARNLSGGY 59  
 DB 67 MKWRTV-VALFVVVVVYLVGVLRALDEQPFESSCKNTALEKAERLRDHICVSP--- 121  
 QY 60 EELERVLRL-LKPRKAGV-----QMRFGSEYFAITVITTTIGYGAAPSTDGK 107  
 DB 122 QLEETLLOHALDADNAGVSPGNSSNNSHMDLGAFFAGTIVITTTIGYGAAPSTDGK 181  
 QY 108 VECMFYALGLIPRLVMPQSLGERINTLVRYLLHRAKKGCLMRADVSMANN-----VLI 162  
 DB 182 IFGLIYALFGLPGLAGIGDQGTIFGKSIAKVER-VFRKQVSGTIRIVISTLEF 239  
 QY 163 GFPGSISTLCIGAAAFSHYEMHTFPQAYYFCITITTTIGFGDYVALQDQALQTOPOXYA 222  
 DB 240 ILACIYFVTLPAIYFKYIEGMLTESIYFVVVLTITVGVGDFVA-GGNAGINREMYKP 298  
 QY 223 FSVYIITGLTVIGAFNLV--VLRFTMNADEKRD-----AEHRALLT 265  
 DB 239 LVWEMILVGLVPAFVAVLSMIGDWLRVLSKTRKEVGEIKAHAAEKANVT 348

RESULT 9  
 ID CINA\_RAT STANDARD: PRT: 538 AA.  
 AC Q9JIS4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 10 (Outward rectifying potassium  
 DE channel protein TREK-2) (TREK-2 K<sup>+</sup> channel subunit).  
 GN KCNK10 OR TREK2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20296807; PubMed-10747911;  
 RA Bang H., Kim Y., Kim D.;  
 RT "TREK-2, a new member of the mechanosensitive tandem-pore K<sup>+</sup> channel  
 RT family";  
 RL J. Biol. Chem. 275:17412-17419(2000).  
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY  
 CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.  
 CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING  
 CC UNSATURATED FREE FATTY ACIDS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,  
 CC AND TESTIS.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF196965; AAF75137.1; -  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003976; Trek\_channel.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 DR PRINTS: PR01499; TREKCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 182 202 POTENTIAL.  
 FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 234 254 POTENTIAL.  
 FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 299 319 POTENTIAL.  
 FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 538 AA; 59800 MW; 1FE33F0AA52B97E4 CRC64;  
 Query Match 17.1%; Score 349.5; DB 1; Length 538;  
 Best Local Similarity 32.8%; Pred. No. 3.2e-20;  
 Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;

QY 1 MKRONVRLALIVCTFTYLLVGAVFDALESEPELIERORLELROOE-LRARNLSGGY 59  
 DB 67 MKWRTV-VALFVVVVVYLVGVLRALDEQPFESSCKNTALEKAERLRDHICVSP--- 121  
 QY 60 EELERVLRL-LKPRKAGV-----QMRFGSEYFAITVITTTIGYGAAPSTDGK 107  
 DB 122 QLEETLLOHALDADNAGVSPGNSSNNSHMDLGAFFAGTIVITTTIGYGAAPSTDGK 181

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Oy 108 FPCMWALGIPALTVMFCOSIGERINTLVRYLLHNAKCGIGRRADYSANN-----VLI 162
Db 102 IFCILYALFGIPDPFFFLAGISIDQGLCTIGFKSIARVEK--YRRKOVSOOTKIRVISTILF 239
Oy 163 GFPSICSTLTCGAAAFASHYEHNTFFQAAVYCCITLTITGFCGDYVALQKQALQOTOPQYVA 222
Db 240 ILAGGIVEVTIPAVIEFKYIEGTWALLESITYFVVVLTITVGGDFVA--CGNAGINRYRMKYP 298
Oy 223 FSVYILGLVYIGAFNLNV--VLRPMYMADEKRD-----AEHRALIT 265
Db 299 LVWFILVGLAVFYFAAVLSMIGDMRLVRSKTKKEEVEGEIKAHAAEWKANVT 348

RESULT 10
CTM4_HUMAN STANDARD: PRT: 393 AA.
ID C1M4_HUMAN
AC 09NYG8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 4 (TWIK)-related archaic acid-
DE stimulated potassium channel protein (TRAAK).
GN KCNK4 OR TRAAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20499203; PubMed=11042359.
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA Kelsell R.E., Muddock P.R., Randall A.D., Rennie G.I., Glozier I.S.,
RT "Cloning, localisation and functional expression of a novel human;
RL cerebellum specific, two pore domain potassium channel.";
RL Brain Res. Mol. Brain Res. 82:74-83(2000).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT chromosome 11.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231699; PubMed=10767409.
RA Lesage F., Maignret F., Lazdunski W.;
RT "Cloning and expression of human TRAAK, a polyunsaturated fatty
RT acids-activated and mechano-sensitive K(+) channel.";
RL FEBS Lett. 471:137-140(2000).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
DR EMBL; AF248242; AAC31731.1; -
DR EMBL; AF247042; AAF64062.1; ALT_INIT.
DR Genew; HGNC:6279; KCNK4.
DR MIM; 605720; -
DR InterPro; IPR001380; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR

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DR InterPro: IPR000636; M+channel\_nlg.  
DR Pfam: PF00520; Ion trans: 1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
KM Ionic channel; transmembrane; Ion transport; Potassium transport;  
KM Glycoprotein.  
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 4 24 POTENTIAL.  
FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).  
FT TRANSMEM 118 138 POTENTIAL.  
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 172 192 POTENTIAL.  
FT DOMAIN 197 221 PORE-FORMING 2 (POTENTIAL).  
FT TRANSMEM 234 254 POTENTIAL.  
FT DOMAIN 255 393 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 328 328 P -> L (IN REF. 2).  
SQ SEQUENCE 393 AA; 42704 MW; 7F1B853A0A9AD57D CRC64;  
  
Query Match 16.1%; Score 329.5; DB 1; Length 393;  
Best Local Similarity 31.0%; Pred. No. 8.5e-19;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;  
  
OY 9 LALVCTFTYLLVAGAVDALESEPE-LIEQRLELROQELRARNYNSO----- 56  
DB 7 LALLLALLVLYVSGVLFRALEPOPEQAOQAELEVERKELRAHCVSDOELGLIKEVA 66  
OY 57 ---GGYELEENVLYLRKPKKAGVOMRFAGSFYFATVTTTTCGYHAASTDGGKVCMEY 113  
DB 67 DALGGADPEPNTSNSSNSHSA---WDGSAFFPSGTTITTCYGNVALRTAGRLFCIFY 123  
OY 114 ALLGIPLVLPFOSIGERINTLVRYLLHRAKKGIGMRAD-----VSMANVLLIG 163  
DB 124 ALVGIPIELGILLAGGDRGLGSLRH-----GIGHLEAIFLKHVPPELVLSAMLEL 176  
OY 164 FFCSITSLICIAAPFSHYEHHTFFQAYYCCITTTTIGFGSDGVVALQDQALOTPOVYAF 223  
DB 177 LIGCLFLVLPFTFPCYIEMDSKLEAIYFVTLITVGFSGYVAGADR--QDSPATQPL 234  
OY 224 SEVYILNG-----LTVIGAFLNLYVLRFTMAAEDEKRDAEHRALLTRNGAGGGGGG 276  
DB 235 VMFPIILGLAVFASVLTITIGMLRVNSR-----TRAEMGGLTAQA 275  
OY 277 GSARTDTAATAAG 292  
DB 276 ASMTGYTAVRYTORAG 291  
  
RESULT 11  
CITM\_MOUSE STANDARD: PRT: 398 AA.  
AC CITM\_MOUSE  
AC 088454;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Potassium channel subfamily k member 4 (TWIK-related arachidonic acid-  
stimulated potassium channel protein) (TRAK).  
DE KCNK4 OR TRAK.  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98292450; PubMed=9628667;  
RA Fluk M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,  
R Lazdunski J.  
RT "A neuronal two p domain k+ channel stimulated by arachidonic acid and  
polyunsaturated fatty acids."  
RL EMBO J. 17:3297-3308(1998).  
RP [2]  
RP ACTIVATION.



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RX MEDLINE-99254548; PubMed-10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND
CC 2/TRUNK/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ARE EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC TESTIS.
CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC FATTY ACIDS. NOT AFFECTED BY VOLTAGE GENERAL ANESTHETICS SUCH AS
CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
DR EMBL: AF056492; AAC40181.1; -
DR MGD: MGI:1298234; Kcnk4.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M-channel_nlg.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein; Alternative splicing.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 PORE-FORMING 1 (POTENTIAL).
FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 119 139 POTENTIAL.
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 198 222 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 63 67 KLVGE -> KAMAI (IN ISOFORM 2).
FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AC92 CRC64;

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Query Match 16.0%; Score 326.5; DB 1; Length 398;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 85; Conservative 45; Mismatches 95; Indels 45; Gaps 7;

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OY 9 LALVCTTYLLVGAAYDALESEPELIERQRL-ROELRARNLSGGYEELRYVL 67
DB 7 LALLLVLLVLSGALVFOALEQPKMDGRQFQPDHPCVSKSLDEPIKILV 66
OY 68 RLKPKAKGVQ-----WRPAGSFYFAITVTITIGYGHAPSTDGKVFCEMFAL 115
DB 67 EALGGANPETSMTSSSHSSAWNGSAFFSGITITITIGIGNLYLHTDAGRLFCIFAL 126
OY 116 LGIPITLVFQSLGERINTLVRYLLHRAKKGIMRA-----DVSMANWVLI 162
DB 127 VGIPLFGLMAGVGRGLTSSLR-----RGIGIEALFLKWHVPGVLRSLSAVLFLI 179
OY 163 GFSCISITLCIGAAGFSLHYEHTPFQAYYCEITLTITGFDYVALQDQALQTPQY-- 220
DB 180 G---CLFVLPITPEVSTYMSKSLAIVFVILTVTGFGDYV--PDGTGQNSPAYOP 234

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OY 221 -----VAFSPYIITGLTIGAFILNLYLR 245
DB 235 LWFEWILFGLAFVASYLVTTIGNWLRVYSRR 264

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RESULT 12

ID	CIVIL_HUMAN	STANDARD	PRF	336 AA.
AC	000180; Q13307;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Potassium channel subfamily K member 1 (inward rectifying potassium channel protein TWIK-1) (Potassium channel KCNK1).			
DE	KCNK1 OR TWIK1 OR HOH1 OR KCNK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.			
RX	TISSUE-Kidney;			
RX	MEDLINE-96183184; PubMed-8605869;			
RA	Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G., Barhanin J.;			
RT	"TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a novel structure.";			
RL	EMBO J. 15:1004-1014(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND REVIEW.			
RC	TISSUE-Brain;			
RX	MEDLINE-98122696; PubMed-9462864;			
RA	Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;			
RT	"Sequence and function of the two P domain potassium channels: implications of an emerging superfamily.";			
RL	J. Mol. Med. 76:13-20(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-98026667; PubMed-9362344;			
RA	Orias M., Velazquez H., Tung F., Lee G., Desir G.V.;			
RT	"Cloning and localization of a double-pore K channel, KCNK1: exclusive expression in distal nephron segments.";			
RL	Am. J. Physiol. 273:F663-F666(1997).			
CC	-1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.			
CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.			
CC	-1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.			
CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
CC	-----			
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CC	-----			
DR	EMBL: U33632; AAB01688.1; -			
DR	EMBL: U76996; AAB97878.1; -			
DR	EMBL: U90065; AAB51147.1; -			
DR	GeneW; HGNC:6272; KCNK1.			
DR	MIM: 601745; -			
DR	InterPro: IPR003280; K+channel_2pore.			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR000636; M-channel_nlg.			
DR	InterPro: IPR001779; TWIK1_channel.			
DR	Pfam: PF00520; Ion_trans; 1.			
DR	PRINTS: PR01333; 2PORECHANNEL.			
DR	PRINTS: PR01096; TWIK1CHANNEL.			

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MOTAGEN 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.  
 SQ SEQUENCE 336 AA; 38143 MW; 2A4ID9501323215D CRC64;  
 Query Match 15.7%; Score 320.5; DB 1; Length 336;  
 Best Local Similarity 32.4%; Pred. No. 3,6e-18;  
 Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9;  
 QY 11 LVYCTFTYLLVGAFAVDALESEBELIERQL-ELRQOELRARNYLSQGYEELERYVLR 69  
 DB 26 LVYGYLLYLVGAFAVSVSELPEDLLRQELRKLRRLEHEHCLSEQLEQLGRLVLEA 85  
 QY 70 KPHKAGV-----QMRAGSFYFAITYITTYTGHAAPSTDGKGVFCMFYALLGIPLT 121  
 DB 86 SMGVSVLSNAGSNMMDFTSALFASVLTGTGHTVPLSGKAFCLITSVIGIPPT 145  
 QY 122 LVWFOSLGERINTLVYLLHRAKGL-----GMRADVSMANVLLGFSCISTLCIG 174  
 DB 146 LLELTAVVORIT-----VHVRRLPVLYFHIRKGFVKQVVAIYHVLGFLVYSCFFPIR 199  
 QY 175 AAASFHYE-HWFFQAVYVCFITLTITGFGDYVA---LQKDALOTOPQVAFSEFYIL 229  
 DB 200 AAFVSLEDDWNELESFECFISLSTIGLDYVPGEGYNQKREL-----YKIGTCYLL 254  
 QY 230 TG---LTVIGAFNLVVL---RFMTNMADEKRDMEH 260  
 DB 255 LGLIAMLVYLETFCLELHKKFRKMFYKKDKDDQVH 292  
 RESULT 13  
 C1W5 HUMAN STANDARD; PRT; 499 AA.  
 AC 095279;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 5 (acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=9903043; PubMed=9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Fauran N.,  
 RA Lazdunski M.;  
 RT Cloning and expression of a novel pH-sensitive two pore domain K+  
 RT channel from human kidney.;  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL  
 CC K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED  
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION  
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL

CC ACIDIFICATION.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF084830; AAC79458.1; -  
 CC Genew: HGNC:6280; KCNK5.  
 CC MIM: 603493; -  
 CC InterPro: IPR003280; K+channel\_2pore.  
 CC InterPro: IPR001622; K+channel\_pore.  
 CC InterPro: IPR000636; M+channel\_nlg.  
 CC Pfam: PF00520; Ion\_trans; 1.  
 CC PRINTS: PR01333; 2PORECHANNEL.  
 CC KMW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 8 26 PORE-FORMING 1 (POTENTIAL).  
 FT DOMAIN 85 112 POTENTIAL.  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT DOMAIN 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.  
 FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DDA00 CRC64;  
 Query Match 15.6%; Score 319; DB 1; Length 499;  
 Best Local Similarity 32.8%; Pred. No. 7,5e-18;  
 Matches 84; Conservative 47; Mismatches 97; Indels 28; Gaps 8;  
 QY 18 YLVGAFAVDALESEBELIE-----RQELRLRQELRARNYLSQGYEELERYV----- 66  
 DB 15 YLVGAFAVDALESEBELIE-----RQELRLRQELRARNYLSQGYEELERYV----- 69  
 QY 67 --LRKPHKAGVOMRAGSFYFAITYITTYTGHAAPSTDGKGVFCMFYALLGIPLTVM 124  
 DB 70 OGVAITGNQTFNMNMNPMIFAATVITTYTGHAAPSTDGKGVFCMFYALLGIPLTVM 129  
 QY 125 POSIGE---RINTVRYLLHRAKGLGMRADVSMANVLLGFSCISTLCIGAAAFSH 180  
 DB 130 ISALGKFFGGRKRLQFL---TKRGVSLRKAQITCTVIFV--KGVHLVIPPVENV 184  
 QY 181 YEHWFQAVYVCFITLTITGFGDYVALQKDALOTOPQVAFSEFYILTGLTVIGAFNL 240  
 DB 185 TEGMNYIEGLYSEFISITIGFGDYFVAGVNPSP-NVHALYRFVELMIVLGLAMLSLFLVN 243  
 QY 241 LVYLRFTNMADEKR 256  
 DB 244 KRVSMFEVHKAIKKR 259  
 RESULT 14  
 C1W1 MOUSE STANDARD; PRT; 336 AA.  
 AC 008581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 1 (inward rectifying potassium channel protein TWIK-1).  
 GN KCNK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97165959; PubMed=9013852;
RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RT Lazdunski M.;
RT "The structure, function and distribution of the mouse TWIK-1 K+
RT channel.";
RL FEBS Lett. 402:28-32(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX MEDLINE=96218573; PubMed=9559671;
RA Arizhig I., Lesage F., Scimeca J.-C., Carle G.-F., Barhanin J.;
RT "Structure, chromosome localization, and tissue distribution of the
RT mouse Twik K+ channel gene.";
RL FEBS Lett. 425:310-316(1998).
CC -1 FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -1 SUBUNIT: HOMODIMER (POTENTIAL).
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM, MODERATE
CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC CORTEX.
CC -1 DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC STABILIZES AFTER DAY 8.
CC -1 MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1 SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL; AF033017; AAC16973.1; .
DR MGD; MGI:109322; Kcnk1.
DR InterPro: IPR0003280; K+-channel_2pore.
DR InterPro: IPR001622; K+-channel_pore.
DR InterPro: IPR000636; M+-channel_nlg.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01096; TWIK1CHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
DR Glycoprotein.
KV DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CANONHD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 336 AA; 82875 MW; A996060A18266FD4 CRC64;
Query Match 15.6%; Score 318.5; DB 1; Length 336;
Best Local Similarity 32.4%; Pred. No.5.2e-18;
Matches 90; Conservative 46; Mismatches 103; Indels 39; Gaps 9;

```

Db	26	LVIGVLLYLVFGAVVSSSELPEDDRLRELRLKRLRLEEHCECSSEQDLPQIGRVLEA	85
Qy	70	KPKHAGY-----QMRPAGSFYATIVITTTIGYGAAPSTDGKFCMFYALLGIPLT	123
Db	86	SNVGSVLSNASGNNMMDEFTSLAFESVTLSTTGGYHVPPLSDGKACACIIVSYGIPFT	145
Qy	122	LWNFQSLGGINLNLVYVLLHRAKKGL-----GMRADVSANNVLLGFSCSLTLCIG	174
Db	146	LLFLTALVAVKQVT-----VAVYRRPVLVYHIRMGFSKQVVALVAVHVLGLFVTVSCFEFIP	199
Qy	175	AAAFSHTE-WMTEFFQAVYCCFTLITLYIGGDYVA-----LQKDALQOTOPQYVAESFYIL	228
Db	200	AAAFSVYLEDMMNLFESFYCFISLSTIGLADIVPREGVNGKREL-----YKIGITCYLL	254
Qy	230	TG---LTVIGAFNLVVL---RFMTMADEKRDPAEH	260
Db	255	IGITMLVLFETFCELHCLKRFRMYVKKDDLDVH	292
RESULT 15			
Clw6	HUMAN	STANDARD:	PRT: 313 AA.
AC	09Y257: 09Hb47:		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Potassium channel subfamily K member 6 (inward rectifying potassium channel protein TWIK-2) (TWIK-originated similarity sequence).		
DE	KCNK6 OR TWIK2 OR TOSS.		
GN	KCNK6 OR TWIK2 OR TOSS.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID:9606;		
NP	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE-Testis:		
RX	MEDLINE=99285568; PubMed=10359073;		
RA	Pountney D.J., Gulkaiov I., Vega-Saenz de Miera E., Holmes D.,		
RT	Saganich M., Rudy B., Artman M., Coetzee W.A.;		
RT	"Identification and cloning of TWIK-originated similarity sequence (TOSS): a novel human 2-pore K <sup>+</sup> channel principal subunit."		
RL	FEMS Lett. 450:191-196(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CYS-53.		
RC	TISSUE-Brain:		
RX	MEDLINE=99175162; PubMed=10075682;		
RA	Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,		
RT	Menta I., Forsythe J.R., Yost C.S.;		
RT	"TWIK-2, a new weak inward rectifying member of the tandem pore domain potassium channel family."		
RL	J. Biol. Chem. 274:7887-7892(1999).		
RN	[3]		
RP	ERRATUM.		
RA	Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,		
RT	Menta I., Forsythe J.R., Yost C.S.;		
RL	J. Biol. Chem. 274:2440-2440(1999).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.		
RX	MEDLINE=20435832; PubMed=10867187;		
RA	Patel A.J., Malingret F., Magnone V., Fosset M., Lazdunski M.,		
RT	Honore E.;		
RT	"TWIK-2, an inactivating 2P domain K <sup>+</sup> channel."		
RL	J. Biol. Chem. 275:28722-28730(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE-Pancreas:		
RA	Strassberg R.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Exhibits outward rectification in a physiological K(+) gradient and mild inward rectification in symmetrical K(+) conditions.		
CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		

Search completed: July 1, 2003, 15:16:07  
Job time : 25 secs

-1 ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are produced by alternative splicing.

-1 TISSUE SPECIFICITY: WIDESPREAD EXPRESSION. DETECTED IN ALL TISSUES TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.

-1 LOWEST EXPRESSION DETECTED IN BRAIN.

-1 MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.

-1 SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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DR	EMBL; AF134149; AAD22980.1;	-
DR	EMBL; AF117708; AAD24000.1;	-
DR	EMBL; AF281302; AAG10506.1;	-
DR	EMBL; AF281303; AAG10507.1;	-
DR	EMBL; BC004367; AAH04367.1;	-
DR	GeneW; HGNC:6281; KCNK6.	
DR	MIM; 603939; -	
DR	InterPro; IPR001632; K+channel_pore.	
DR	InterPro; IPR000636; M+channel_nlg.	
DR	InterPro; IPR001779; TWIK1_channel.	
DR	Pfam; PF00520; Ion_trans_1.	
DR	PRINTS; PR01096; TWIKCHANNEL.	
KM	Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing.	
FT	DOMAIN	1 4
FT	TRANSSEM	5 25
FT	DOMAIN	90 115
FT	TRANSSEM	121 141
FT	DOMAIN	142 172
FT	TRANSSEM	173 193
FT	DOMAIN	199 223
FT	TRANSSEM	236 256
FT	DOMAIN	257 313
FT	CARBOHYD	79 79
FT	CARBOHYD	85 85
FT	VARSPLIC	1 134
FT	MUTAGEN	53 53
SO	SEQUENCE	313 AA; 33747 MW; 1379382DBF0575DE CRC64; C>A; NO CHANNEL ACTIVITY.

Query Match	14.58	Score 295.5	DB 1	Length 313
Best Local Similarity	31.78	Pred. No. 3.1e-16		
Matches 90	Conservative 40	Mismatches 95	Indels 59	Gaps 12

QY 18 YLLVGAAYVDALAESEPELEERLRLROOELRARN-----LSOGYELE 63  
 Db 17 YIVIGALLVARLEGPEARLRARELETLRQQLQSRPCVAARALDAFVERVLAAG---RLG 73  
 QY 64 RYVLRRLKPKHQAQV---WRPAGSEYPAITVTTTGYGAADSTDGKVCFFMVALGIPL 120  
 Db 74 RYVLAANSAGSANSADPAMPDFASALFFASTLITVWGQYETTELDPAGAKFASIAFPALLGPT 133  
 QY 121 TLVWFOSLGERINTLRYLLTHRAKKGGLG-----RRADVSMANWVLIIGFSCSTLC-- 172  
 Db 134 TMLLRASQRLSL---LTHVPLSMLSRMGCHPRRA-----ACNHLVALLGVVYVTCFL 186  
 QY 173 IGAAPASHYEH-WTFEQAYVYCFITLWTIGFGDYVALQKDALQALQTOPQ---YVAFSFVYI 228  
 Db 187 VPVAVIAHLEAMSFELDAFYCFISLSTGLGDYVGR---AGQPYRALYKVLVTVYL 242  
 QY 229 LRGLT-----VIGAFILNVLVLRMT-----MAADEKR 256  
 Db 243 FLGLVAMVLVLOTFRHVSDLHGLCTELLILPPCCPASFVADDDR 286

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:13:42 ; Search time 35 Seconds  
(without alignments)  
2319.502 Million cell updates/sec

Title: US-09-939-484-4  
Perfect score: 2042  
Sequence: 1 MKRONVRLTALIVCTFTYLL.....STGLHSLSFRLMKRRSSV 394

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_podent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	84.8	392	11	Q9ESM5
2	1333	65.3	299	11	Q9OX34
3	1298.5	63.6	301	11	Q9ESM4
4	999	48.9	396	11	Q923V6
5	960.5	47.0	395	11	Q9JUD4
6	924	45.2	237	11	Q9ES08
7	916.5	44.9	318	11	Q9RS10
8	846	41.4	330	4	Q9HBC8
9	838	41.0	330	4	Q9H427
10	820	40.2	329	5	Q17185
11	777	38.1	340	5	Q9VHE0
12	742	36.3	398	5	Q9VFS9
13	732.5	35.9	270	11	Q9JLS7
14	690.5	33.8	237	11	Q920G1
15	599	29.3	364	5	Q76790
16	373	18.3	405	11	Q8RI15

17	369	18.1	405	11	Q9ERS0	Q9ERS0	rattus norv
18	367	18.0	426	11	Q920B6	Q920B6	rattus norv
19	363	17.8	411	4	Q9NPT2	Q9NPT2	homo sapien
20	361	17.7	294	4	Q9H591	Q9H591	homo sapien
21	361	17.7	309	4	Q96T55	Q96T55	homo sapien
22	358	17.5	408	4	Q96E79	Q96E79	homo sapien
23	357.5	17.5	408	4	Q9HB14	Q9HB14	homo sapien
24	349.5	17.1	543	4	Q8TDX8	Q8TDX8	homo sapien
25	349.5	17.1	543	4	Q8TDX7	Q8TDX7	homo sapien
26	329.5	16.1	419	4	Q96T94	Q96T94	homo sapien
27	325	15.9	498	5	Q22940	Q22940	caenorhabdi
28	324	15.9	502	11	Q9JRK62	Q9JRK62	mus muscicu
29	319.5	15.6	336	11	Q922T2	Q922T2	rattus norv
30	319.5	15.6	336	11	Q99199	Q99199	mus muscicu
31	319	15.6	397	11	Q924I4	Q924I4	rattus norv
32	317.5	15.5	336	11	Q8R454	Q8R454	rattus norv
33	310.5	15.2	430	4	Q9HB15	Q9HB15	homo sapien
34	309.5	15.2	430	11	Q9ERS1	Q9ERS1	rattus norv
35	302	14.8	259	6	Q02821	Q02821	oryctolagus
36	294.5	14.4	332	4	Q96T54	Q96T54	homo sapien
37	294.5	14.4	332	4	Q8TAW4	Q8TAW4	homo sapien
38	293	14.3	393	5	Q9XU07	Q9XU07	caenorhabdi
39	288	14.1	229	4	Q9H592	Q9H592	homo sapien
40	288	14.1	343	4	Q9BXD1	Q9BXD1	homo sapien
41	281.5	13.8	385	5	Q9VYV5	Q9VYV5	drosophila
42	278.5	13.6	592	5	Q9W4G2	Q9W4G2	drosophila
43	278.5	13.6	995	5	Q9W2L7	Q9W2L7	drosophila
44	276.5	13.5	313	11	Q9ERU5	Q9ERU5	rattus norv
45	275	13.5	524	5	Q21729	Q21729	caenorhabdi

## ALIGNMENTS

## RESULT 1

Q9ESM5 PRELIMINARY; PRT; 392 AA.  
ID Q9ESM5  
AC Q9ESM5;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE TASK1 splice bvariant (TASK1b).  
GN KCNK3B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid-10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Ohya S., Kitakawa M., Imaizumi Y.;  
RT "TASK1 splice bvariant (TASK1b) (KCNK3b).";  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AB048823; BAB16710.1;  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR InterPro: IPR003092; TASK\_channel.  
DR Pfam; PF00520; Ion\_trans\_1.  
DR PRINTS; PRO1333; 2PORECHANNEL.  
DR PRINTS; PRO1584; TASKCHANNEL.  
DR PRINTS; PRO1095; TASKCHANNEL.  
SQ SEQUENCE 392 AA; 43150 MW; F5438B12A0D7FB1B CRC64;

Query Match 84.8%; Score 1732; DB 11; Length 392;  
Best Local Similarity 83.9%; Pred. No. 1.8e-153;  
Matches 345; Conservative 7; Mismatches 23; Indels 36; Gaps 4;

Qy 1 MKRONVRLTALIVCTFTYLLGVAVFDALESEPELIERQRLRNOQLRARNYSOGYE 60  
|||  
Db 1 MKRONVRLTALIVCTFTYLL.....LES-----ELQMLELRARNYNSSEGYE 41  
Qy 61 ELERVLRLKPKAGVQWRFGSFYFAITVTTIGYGHAPSTDGKRVCFMVALGIPL 120

```

DB 42 EERRVLRKPKHAGVOMRAGSFYFAITVITIGYGHAPSTDGKVFCEMFAALGIP 101
OY 121 TLVMPFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCISITLIGAAAFSH 180
DB 102 TLVMPFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCISITLIGAAAFST 161
OY 181 YEHMFEFOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLLTGLTIGAFILN 240
DB 162 YEHMFEFOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLLTGLTIGAFILN 221
OY 241 LVYLRMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA- 291
DB 222 LVYLRMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA- 281
OY 292 -----GGGGRNRYAEVLHFOQSMCCLWYKSRKLOYSTPMITPRDSTSDTCVEOS 343
DB 282 GKVGVGVGSGGRNRYAEVLHFOQSMCCLWYKSRKLOYSTPMITPRDSTSDTCVEOS 341
OY 344 HSPGGGGRYSDTPSRRLCSGAPRAISVSTGLSLSTFNGLMKRSSV 394
DB 342 HSPGGGGRYSDTPSRRLCSGAPRAISVSTGLSLSTFNGLMKRSSV 392

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## RESULT 2

```

OY 090X34 PRELIMINARY; PRT; 299 AA.
AC 090X34:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative potassium channel DP4 (Fragment).
GN KCNK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K.;
RU Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB022821; AAD09338.1; -.
DR MGD; MGI:1100509; Kcnk3.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1333; 2PORKCHANNEL.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW Ionic channel.
FT NON_TER 1
FT NON_TER 299
SQ SEQUENCE 299 AA; 33325 MW; DCD41DBA212939C4 CRC64;

```

Query Match 65.3%; Score 1333; DB 11; Length 299;  
 Best local similarity 88.9%; Pred. No. 2.5e-116;  
 Matches 263; Conservative 7; Mismatches 18; Indels 8; Gaps 1;

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OY 4 QNVRTLALIVCTFTYLLVGAAVFDALSEPELIERORLELROELRARNVLSGGYEEL 63
DB 2 ENVRTLALIVCTFTYLLVGAAVFDALSEPELIERORLELROELRARNVLSGGYEEL 61
OY 64 RYVLRKPKHAGVOMRAGSFYFAITVITIGYGHAPSTDGKVFCEMFAALGIP 123
DB 62 RYVLRKPKHAGVOMRAGSFYFAITVITIGYGHAPSTDGKVFCEMFAALGIP 121
OY 124 MFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCISITLIGAAAFSH 183
DB 122 MFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCISITLIGAAAFST 181

```

```

OY 184 WFEFOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLLTGLTIGAFILN 243
DB 182 WFEFOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLLTGLTIGAFILN 241
OY 244 LREMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA 291
DB 242 LREMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA 297

```

## RESULT 3

```

OY 09ESM4 PRELIMINARY; PRT; 301 AA.
AC 09ESM4:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE TWIK-related acid-sensitive K+ channel splice variant (TASK1c).
GN KCNK3c.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohya S., Kitsuawa M., Imaizumi Y.;
RA TISSUE=AOIRA;
RT "TWIK-related acid-sensitive K+ channel (TASK1) (KCNK3) splice
RT variant.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB048824; BAB16711.1; -.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 301 AA; 32811 MW; 265DE38DFA79595E CRC64;

```

Query Match 63.6%; Score 1298.5; DB 11; Length 301;  
 Best local similarity 85.0%; Pred. No. 4.2e-113;  
 Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2;

```

OY 111 MFYALIGIPLVMPFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCIST 170
DB 1 MFYALIGIPLVMPFOSIGERTLVRYLLHRAKRGIGRRADVSNANNVLTGFEFCIST 60
OY 171 LCIGAAAFSHEMTFEOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLL 230
DB 61 LCIGAAAFSHEMTFEOAYVYCFITLTTIGFDYVALQKDALQTOPQVAFSFIYLL 120
OY 231 GLTVIGAFILNVLVLRMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTT 282
DB 121 GLTVIGAFILNVLVLRMTNNAEDKDAEHRALLTRNGOAGGGG-----GGSAAHTT 180
OY 283 DRASSTAA-----GGGGRNRYAEVLHFOQSMCCLWYKSRKLOYSTPMITPRDL 333
DB 181 DRYTCAAAAGMGVGVGSGGRNRYAEVLHFOQSMCCLWYKSRKLOYSTPMITPRDL 240
OY 334 STSDTCVEOSHSPGGGRYSDTPSRRLCSGAPRAISVSTGLSLSTFNGLMKRSS 393
DB 241 STSDTCVEOSHSPGGGRYSDTPSRRLCSGAPRAISVSTGLSLSTFNGLMKRSS 300
OY 394 V 394
DB 301 V 301

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## RESULT 4

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OY 0923V6 PRELIMINARY; PRT; 396 AA.
AC 0923V6:
DT 01-DEC-2001 (Tremblrel. 19, Created)

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RP SEQUENCE FROM N.A.
RA Lovell J.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Preisig-Mueller R., Rajan S., Derst C.;
RT "Cloning and sequencing of a novel tandem pore domain potassium
   channel (TASK-4).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A119522; CAC14068.1; -
DR EMBL; AF294352; AAK97093.1; -
DR EMBL; AF294351; AAK97092.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans.1.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KM Ionic channel.
SQ SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;

Query Match 41.0%; Score 838; DB 4; Length 330;
Best Local Similarity 64.3%; Pred. No. 5.2e-70;
Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;

QY 1 MKRQNVTLALIVCTFTYLLVGAVPDALESEPELIRQRLERQDELRLARYNLSSGGE 60
DB 1 MKRPVNAAGLVCTCTCYLLVGAVPDALESESGRQLLYOKRGALRRKFGFSADYR 60

QY 61 ELERVNRLKPKHAGVOMRFGSGFYFAITVITTYIGYHAPSTGKVFQCFYALLGIP 120
DB 61 ELERLALQAPRHARGRMKPGSFYFAITVITTYIGYHAPSTGKVFQCFYALLGIP 120

QY 121 TLVFGSLGERINTLVYLLHRAKKGIMRADVSMANMVLIGFSCISTLCIGAAFSH 180
DB 121 TLVTFOSLGERLNAVYRLLAACCCGLRMTCVSTNLVAVAGLCAATLALGAFAFSH 180

QY 181 YEHWTFQAYVYCCFTLTITGFGDYVALQKDALQOPQVAVSEFVILGLTVIGAF 240
DB 181 FECHTFPHAYVYCCFTLTITGFGDYVALQSGEALQKRLPYAVSEFTLILGLTVIGAF 240

QY 241 LVVLRFTMNAEDEKRD 258
DB 241 LVVLRFLVASADMPERAA 258

RESULT 10
ID 017185 PRELIMINARY; PRT; 329 AA.
AC 017185; 076795;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 37.0 kDa protein (Putative potassium channel subunit
   n2p38).
GN F34D6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OC NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; Pubmed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
   investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-20196006; Pubmed-10731132;
RA Murray J., Wohldmann P., O'Neal D.;

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RT "The sequence of C. elegans cosmid F34D6.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salkoff L.;
RT "Potassium channels in C. elegans.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF025454; AAC71151.2; -
DR EMBL; AF083652; AAC32863.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans.1.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KM Hypothetical protein; Ionic channel.
SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;

Query Match 40.2%; Score 820; DB 5; Length 329;
Best Local Similarity 48.3%; Pred. No. 2.5e-68;
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;

QY 1 MKRQNVTLALIVCTFTYLLVGAVPDALESEPELIRQRLERQDELRLARYNLSSGGE 60
DB 1 MKRQNVTLALIVCTFTYLLVGAVPDALESEPELIRQRLERQDELRLARYNLSSGGE 60

QY 61 ELERVNRLKPKHAGVOMRFGSGFYFAITVITTYIGYHAPSTGKVFQCFYALLGIP 120
DB 61 ELERVNRLKPKHAGVOMRFGSGFYFAITVITTYIGYHAPSTGKVFQCFYALLGIP 120

QY 121 TLVFGSLGERINTLVYLLHRAKKGIMRADVSMANMVLIGFSCISTLCI--GAAAF 178
DB 121 GLIFOSIGERINTLVYLLHRAKKGIMRADVSMANMVLIGFSCISTLCI--GAAAF 178

QY 179 SHEHWTFQAYVYCCFTLTITGFGDYVALQKDALQOPQVAVSEFVILGLTVIGAF 238
DB 178 SSYENMTYFDVAVYCCFTLTITGFGDYVALQKRSIQTOPEYVFSFLIFGLTVISAA 237

QY 239 LNVVLRFTMNAEDEKRDHRAAL---LTRNGAGGGGGGCAHTTDRASSTAAAGG 294
DB 238 MNLVLRFTMNAEDEKRDDEALIAAGLVRVGDPTADDFGLPLSDNVSLAS----- 292

QY 295 GFRVVAEVLHFGSGCLMWKSKREKLOYSLPIIPDLSTSDCVFQSSSPGCG 350
DB 293 -----CSC-YQLPDEKLHR-----HRKHTPEHGG 316

RESULT 11
ID 09VHEO PRELIMINARY; PRT; 340 AA.
AC 09VHEO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG9361 protein.
GN CG9361.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; Pubmed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.;

```

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu D., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Moberly C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003682; AAF54374.1; -  
 DR FlyBase: FBgn0037690; CG9361.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR PRINTS: PRO1586; THIRCHANNEL.  
 DR SEQUENCE 340 AA; 37840 MW; 018D756D21F8D57A CRC64;

Query Match 38.1%; Score 777; DB 5; Length 340;  
 Best Local Similarity 47.7%; Pred. No. 2.7e-64;  
 Matches 166; Conservative 48; Mismatches 118; Indels 16; Gaps 5;

QY 1 MKRONVRLTALIVCTFTYLLVGAANVDALESEBELTERORLELROQELRARNYLSGGYE 60  
 DB 2 MKRONVRLTSLVCTFTYLLVGAANVDALESEBELTERORLELROQELRARNYLSGGYE 61  
 QY 61 ELERVVLRLKPKRAGQAFAGSFYATVITTTIGGHAAPSTDGKVCVCMFYALGIFL 120  
 DB 62 VNEIYIENKPKRAGQAFAGSFYATVITTTIGGHAAPSTDGKVCVCMFYALGIFL 121  
 QY 121 TLVNFOSLGERINTLVRLYLHRAKKGILGRADVSANVNL-IGFSCSTLTCIGAAAS 179  
 DB 122 GLVNFOSLGERINTLVRLYLHRAKKGILGRADVSANVNL-IGFSCSTLTCIGAAAS 180  
 QY 180 HVEHMTFOAYYYCFTLTTLTIGFDVALOKDOALOTOPQYVAFSEVYLLTGLTVIGAF 239  
 DB 181 RREGMSYFDSFYCFYTLTTLTIGFDVALOKDOALOTOPQYVAFSEVYLLTGLTVIGAF 240  
 QY 240 NLVVLRFMTMADEKRAEHRALLTRNGAGGGGGGSAHTTTRASTAAAGGGGFRNV 299  
 DB 241 NLVVLRFMTMADEKRAEHRALLTRNGAGGGGGGSAHTTTRASTAAAGGGGFRNV 299  
 QY 300 Y-AYVLHFGMSCLMYKSRKRL-YSIPMIIPRDLSTSDTCVDS 343

DB 291 YTTENDETASLSCCTCGMGTGCTCLNHEQFVDPDFQPTDITESTICLKRA 338  
 RESULT 12  
 ID Q9VES9 PRELIMINARY; PRT; 398 AA.  
 AC Q9VES9;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE CG9637 protein.  
 GN CG9637.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
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 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
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 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
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 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
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 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Moberly C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003701; AAF54970.1; -  
 DR FlyBase: FBgn0038165; CG9637.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR SEQUENCE 398 AA; 44269 MW; D5DC011E9BDA6D7E CRC64;

Query Match 36.3%; Score 742; DB 5; Length 398;  
 Best Local Similarity 42.8%; Pred. No. 6.2e-61;  
 Matches 161; Conservative 65; Mismatches 76; Indels 74; Gaps 9;

QY 1 MKRONVRLTALIVCTFTYLLVGAANVDALESEBELTERORLELROQELRARNYLSGGYE 60



DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)  
DE Putative potassium channel subunit N2P20.  
GN TWK-4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_Taxid-6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang Z.-W., Salkoff L.;  
RT "Potassium channels in C. elegans";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hembry C.;  
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-99069613; PubMed-9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL: AF083646; AAC32857.1; -  
DR EMBL: Z70266; CAB61045.1; -  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR Pfam: PF00520; Ion.trans.1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
KW Ionic channel.  
SQ  
SEQUENCE 364 AA: 41374 MW: 4247A6050CCCA313 CRC64;  
  
Query Match 29.3%; Score 599; DB 5; Length 364;  
Best Local Similarity 46.1%; Pred. No. 1.3e-47;  
Matches 119; Conservative 46; Mismatches 81; Indels 12; Gaps 3;  
  
QY 4 QNVRTLALIVCTFTYLLVGAAYFDALSEPELIERQRLERQELRARNLSQGYEELD 63  
DB 7 KSRALLILSTFTYLLFGAMVFDKLESEKDTWVRDEIRITDRLKHKNFSEBDLHFE 66  
QY 64 RYVLRKPKHKAQVQWRFAQSFYFAITVTITIGYGHAPSTDGKVPQCMFYALLGPIPLIV 123  
DB 67 AIAIKSIPQAGIQWQFAGAFYFAIVITTVGIGHAPSTNAGKLCMTFALGVPMLI 126  
QY 124 MFQSLGERINTLVRYLLHRAKKGMR---RADVSMANMVL---IGFFSCISTLCIGA 175  
DB 127 MFQSLGERINTLVRYLLHRAKKGMR---RADVSMANMVL---IGFFSCISTLCIGA 175  
QY 176 AAFSHREHWTFPQAYYCFITLTITIGFGDYVALQKDALQTOPQYVAFSEFVYILGLTVI 235  
DB 183 YMFHTLEKWSIFDAYFCMITEFTSTIGFGDVLPLQGVNALQDQPLVYFATIMFTLGLAVF 242  
QY 236 GAFINLVVLRKMTMAED 253  
DB 243 SACVNLVLGFMASNADE 260

Search completed: July 1, 2003, 15:19:23  
Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:14:17 ; Search time 18 Seconds  
(without alignments)  
2104.276 Million cell updates/sec

Title: US-09-939-484-4

Sequence: 1 MKRONVRLTLIVCTFTYLL.....STGLHSLSLTFRGLMKRRSSV 394

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	41.4	330	2	JC7703 TASK-5 protein - h
2	820	40.2	329	2	T43509 probable potassium
3	806.5	39.5	336	2	T432347 outward rectifier
4	599	29.3	334	2	T19860 hypothetical prote
5	599	29.3	364	2	T43361 probable potassium
6	320.5	15.7	336	2	S65566 inward rectifier p
7	307.5	15.1	513	2	T28933 hypothetical prote
8	293	14.3	393	2	T25392 hypothetical prote
9	276.5	13.5	1910	2	H88124 protein T12C9.3 [1
10	275	13.5	524	2	T23907 hypothetical prote
11	268	13.1	1539	2	T30037 hypothetical prote
12	262	12.8	443	2	T21598 hypothetical prote
13	261.5	12.8	1001	2	T13807 potassium channel
14	258.5	12.7	335	2	S44635 T22b7.7 protein -
15	258.5	12.7	427	2	T27681 hypothetical prote
16	258	12.6	383	2	T23182 hypothetical prote
17	256.5	12.6	452	2	T21118 hypothetical prote
18	251	12.3	544	2	T43364 potassium channel
19	251	12.3	576	2	T43363 potassium channel
20	250	12.2	569	2	T43531 probable potassium
21	248	12.1	444	2	T26229 hypothetical prote
22	247.5	12.1	392	2	T45032 hypothetical prote
23	245	12.0	769	2	T27550 hypothetical prote
24	244	11.9	381	2	T43393 potassium channel
25	243	11.9	528	2	T21834 hypothetical prote
26	239.5	11.7	522	2	T24265 hypothetical prote
27	235.5	11.5	475	2	T27725 hypothetical prote
28	234.5	11.5	485	2	T24201 hypothetical prote
29	231.5	11.3	484	2	T43529 probable potassium

30	231.5	11.3	519	2	T16629 hypothetical prote
31	229	11.2	325	2	T15584 hypothetical prote
32	229	11.2	461	2	T43394 potassium channel
33	222.5	10.9	600	2	T24626 hypothetical prote
34	216	10.6	350	2	T15178 hypothetical prote
35	215.5	10.6	643	2	T26616 hypothetical prote
36	211	10.3	539	2	T23700 hypothetical prote
37	210.5	10.3	504	2	T23269 hypothetical prote
38	210	10.3	1136	2	T26953 hypothetical prote
39	205.5	10.1	586	2	T21683 hypothetical prote
40	201.5	9.9	551	2	T16426 hypothetical prote
41	201.5	9.9	555	2	T43357 potassium channel
42	200.5	9.8	700	2	T27364 hypothetical prote
43	199.5	9.8	660	2	T21551 hypothetical prote
44	193.5	9.5	523	2	T23373 hypothetical prote
45	190.5	9.3	383	2	T23746 hypothetical prote

ALIGNMENTS

RESULT 1  
JC7703  
TASK-5 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: JC7703  
R:Kim, D.; Gnatenco, C.  
Biochem. Biophys. Res. Commun. 284, 923-930, 2001  
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.  
A:Reference number: JC7703; MUID:21303050; PMID:11409881  
A:Accession: JC7703  
A:Molecule type: DNA  
A:Residues: 1-330 <KIN>  
A:Cross-references: GB:AL118522  
A:Comment: This protein, a new member of the tandem-pore K+ channel family with four hormone secretion, but does not produce a functional plasma membrane K+ current by it C:Genetics:  
A:Gene: Task-5  
A:Map position: 20q12  
C:Keywords: transmembrane protein  
F:7-30/Domain: transmembrane segment #status predicted <TMS1>  
F:107-158/Domain: transmembrane segment #status predicted <TMS2>  
F:126-155/Region: hydrophobic cytoplasmic linker #status predicted  
F:156-180/Domain: transmembrane segment #status predicted <TMS3>  
F:220-240/Domain: transmembrane segment #status predicted <TMS4>  
Query Match 41.4% Score 846; DB 2; Length 330;  
Best Local Similarity 64.7% Pred. No. 1.7e-69;  
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;  
OY 1 MKRONVRLTLIVCTFTYLLVGAAYDVALESEPELIERORLELRQELRARNLSQGYE 60  
DB 1 MRRPSVRAAGLVLCYLVGAAYFDVALESEAGSORLLVQKRRRFGSAEDYR 60  
OY 61 ELERVVLTKRKKGVCQRFAGSEFATVTTTGGYGAASSTOGKRFCHFYALGIP 120  
DB 61 ELERVVLTKRKKGVCQRFAGSEFATVTTTGGYGAASSTOGKRFCHFYALGIP 120  
OY 121 TLVVFOSGERINTLVRYLTHRAKKGGLRRADVSMMANNVILGFSCISTCIGAAFSH 180  
DB 121 TLVVFOSGERINTLVRYLTHRAKKGGLRRADVSMMANNVILGFSCISTCIGAAFSH 180  
OY 181 YEHMTFFQAYYYCFITLTTFGGDYVALQDQALQTOPQYVAFSEVYLTGLVYIGAF 240  
DB 181 YEHMTFFQAYYYCFITLTTFGGDYVALQDQALQTOPQYVAFSEVYLTGLVYIGAF 240  
OY 241 LVVLRFTMNADEKRD 258  
DB 241 LVVLRFTMNADEKRD 258  
OY 258 LVVLRFTMNADEKRD 258  
DB 258 LVVLRFTMNADEKRD 258  
RESULT 2





A:Accession: T23592  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393 <MIL>  
A:Cross-references: EMBL:292813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1  
A:Experimental source: clone T28A8  
C:Genetics:  
A:Gene: CESP:T28A8.1  
A:Map position: 3  
A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match 14.3%; Score 293; DB 2; Length 393;  
Best Local Similarity 26.6%; Pred. No. 7.7e-19;  
Matches 78; Conservative 57; Mismatches 96; Indels 62; Gaps 9;

OY 9 LALIVCTFTYLVGAAPFALESEPEL-----IERQRLERL----- 45  
DB 15 VSLIVSVYVYGALFLYQLEOPNEVARNIERPNHKKOMIEHLMEMRESGIGHV 74  
OY 46 -DELARY--NLSQGYEELERVLRKPKAG-----VQWRFGSFFAIVITTYG 97  
DB 75 VEDLAVKYVDNVRILFEAFDFHCIGAKHLRPGCEDDYNNMTALFFTTLLTIGYG 134  
OY 98 HAAPSTDGKVFQMTYALLGIPFLVMFQSLGERI--NTLVRYLHR----- 142  
DB 135 NLTPVYGRKLLCILALFGVPLILTVADIGKFLSENIVQLTWYRKLEKCSKOKYSV 194  
OY 143 -AKKGGMRRADY--MANMVLIGFSCS-----STLCGAANFSYEHHTFQAYYCP 194  
DB 195 ISKDKRKEGDLNDHLENYISIPFLVAILSTTTGAVVLSMEGDFSGFYFSF 254  
OY 195 ITLTITGFDYVALQDQALQTOPQYVAFSEFVYILGLVYGAFLNVLVRFM 247  
DB 255 IFMTVTGFGDIYELKR-----EYIIDLCTIIIGLSTTMCIDLVIQYI 299

RESULT 9  
Protein T12C9.3 (imported) - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: H88124  
R:anonymous, The C. elegans Sequencing Consortium.  
A:title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; WID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: H88124  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <STO>  
A:Cross-references: GB:chr\_II; PIDN:AC71141.1; PID:q1086770; GSPDB:GN00020; CESP:T12C9.3  
C:Genetics:  
A:Gene: T12C9.3  
A:Map position: 2

Query Match 13.5%; Score 276.5; DB 2; Length 1910;  
Best Local Similarity 23.3%; Pred. No. 1.7e-16;  
Matches 80; Conservative 49; Mismatches 107; Indels 107; Gaps 8;

OY 4 QNVRTLA-----LIVCTFTYLVGAAPFALES--EPELIERORLEROELBARYN 53  
DB 189 QNIRKAKLALPHIVVVCVCIATIGAMIFTYLSPEDRLKETGRKTIABRSNLTK 248  
OY 54 LS-----OGGYEELERV--VL 67  
DB 249 INNKEKVMKEDIEKELMLYSEKLYAKFQYVRYSDVPTIGEGSSSYEADETGDSB 308  
OY 68 RLKPKHAG-----VQWRFGSFFAIVITTYGHAAPSTDGKVFQYFALLGI 118  
DB 309 RRRHRHGNKRGDRGSEKMMYTSALFPAATMATIGNIVPFLGRLACVLFALFGA 368

OY 119 PLTLVNFQSLGERINTLVRYLHRKAKG-----LGMRRADYS 155  
DB 369 PIALITIGDKFLSCTITMLYKMKRGSRLDSAMKRRFGLEDISIDLESASKNODS 428  
OY 156 MANM-----VLIGFSCISTLCGAANFSYEHHTFQAYYCEITLTIGFGD 204  
DB 429 ILDMDEIDKSEVPLVWFTTLLVYAFGGLFSLIEMWSYADAFYSFISLTIGFGD 488  
OY 205 YVALQDQALQTOPQYVAFSEFVYILGLVYGAFLNVLVRFM 247  
DB 489 IYFENHD-----YIALMLYLVGSLSTTMCIDLVIQYI 523

RESULT 10  
T23907  
hypothetical protein R04F11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23907  
R:Harris, B.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19816  
A:Accession: T23907  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-524 <MIL>  
A:Cross-references: EMBL:274475; PIDN:CAA8957.1; GSPDB:GN00023; CESP:R04F11.4  
A:Experimental source: clone R04F11  
C:Genetics:  
A:Gene: CESP:R04F11.4  
A:Map position: 5  
A:Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2

Query Match 13.5%; Score 275; DB 2; Length 524;  
Best Local Similarity 23.3%; Pred. No. 4.8e-17;  
Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;

OY 11 LIVCTFTYLVGAAPFALESEPELIERORLEROELRARY----- 52  
DB 18 LVLLSIGTYLIGALCFHHYKREYEQQLRNETSRIGELKRVNDQLMBSNNGTAVSTM 77  
OY 53 NLSQGYEELERVVL-----RLKPH-----KAGVWRFGSFFAIVITTYGHAAP 101  
DB 78 QFANDMDDELIRVDYFDTFRNMYTPDDVIYGDGPIKMSFMSIFSWTAITTYGHIYP 137  
OY 102 STDGKVFQCFYALLGIPFLVMFQSLGERINTLV----- 136  
DB 138 RTDEGRVAILFYALLGIPFLVTVADIGRLATYIILHGYMAVSEVYNSCLKICIKMA 197  
OY 137 -----RY-----LHRAKK-----GLGMR----- 150  
DB 198 CCMIRLPKRHIIMPTIELLQRTQKLPNNNNPVAATAASAGGTRRRKKQQRDNVSDAG 257  
OY 151 -----TFDNISEINDSGENENGEDEEQIQDPNSHKEKRVSLFTLLIMLGY-----VAGG 311  
DB 258 TFDNISEINDSGENENGEDEEQIQDPNSHKEKRVSLFTLLIMLGY-----VAGG 311  
OY 175 AAASFHYEHHTFQAYYCEITLTIGFGDYVALQDQALQTOPQYVAFSEFVYILGLV 234  
DB 312 AYIYRWEMETFEAFYFCFVYVTTTIGFDIVPAND-----WLPATLAIYVGLII 363  
OY 235 IGAFLNVL 242  
DB 364 TTMCIDLV 371

RESULT 11  
T30037  
hypothetical protein F20A1.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T30037





C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Sep-1997  
C:Accession: S44635  
R:Anderson, K.  
submitted to the EMBL Data Library, March 1993  
A:Description: Sequence Of the C. elegans cosmid F22B7.  
A:Reference number: S44628  
A:Accession: S44635  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-335 <AND>  
A:Cross-references: EMBL:L12018; NTD:g156298; PID:g156306  
C:Genetics:  
A:Introns: 18/3; 79/1; 131/2; 173/3; 251/3

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:15:48 ; Search time 26 Seconds  
(without alignments)  
1661.571 Million cell updates/sec

Title: US-09-939-484-4  
Perfect score: 2042  
Sequence: 1 MKRONVRLTALIVCTFTYLL.....STGLHSLSTRGLMKRRSSV 394

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	10 US-09-939-484-4	Sequence 4, Appl1
2	2042	100.0	394	10 US-09-939-483-4	Sequence 2, Appl1
3	2042	100.0	394	10 US-09-798-584-15	Sequence 15, Appl1
4	1819	89.1	405	10 US-09-939-484-5	Sequence 5, Appl1
5	1819	89.1	405	10 US-09-939-483-5	Sequence 5, Appl1
6	1278	62.6	258	10 US-09-746-491-61	Sequence 61, Appl1
7	1116	54.7	374	10 US-09-798-584-1	Sequence 1, Appl1
8	1069.5	52.4	365	10 US-09-746-491-60	Sequence 60, Appl1
9	846	41.4	330	10 US-09-746-491-59	Sequence 59, Appl1
10	838	41.0	330	10 US-09-746-491-58	Sequence 58, Appl1
11	838	41.0	330	10 US-09-746-491-57	Sequence 57, Appl1
12	774	37.9	279	10 US-09-746-491-22	Sequence 22, Appl1
13	370	18.1	370	10 US-09-864-761-34389	Sequence 34389, A
14	370	18.1	370	10 US-09-939-484-8	Sequence 8, Appl1
15	369	18.1	411	10 US-09-939-483-8	Sequence 8, Appl1
16	363	17.8	411	9 US-09-828-746-6	Sequence 6, Appl1
17	363	17.8	411	9 US-10-121-746-63	Sequence 83, Appl1
18	361	17.7	294	9 US-09-828-746-2	Sequence 2, Appl1
19	349.5	17.1	526	10 US-09-729-920-4	Sequence 4, Appl1

20	349.5	17.1	538	10 US-09-729-920-5	Sequence 5, Appl1
21	349.5	17.1	543	10 US-09-729-920-2	Sequence 2, Appl1
22	329.5	16.1	392	10 US-09-747-835A-55	Sequence 55, Appl1
23	329.5	16.1	393	9 US-10-243-035-2	Sequence 2, Appl1
24	329.5	16.1	419	10 US-09-828-035-2	Sequence 2, Appl1
25	329.5	16.1	419	10 US-09-747-835A-29	Sequence 29, Appl1
26	320.5	15.7	336	9 US-10-205-823-190	Sequence 190, App
27	320.5	15.7	336	10 US-09-939-484-2	Sequence 2, Appl1
28	320.5	15.7	336	10 US-09-939-483-2	Sequence 2, Appl1
29	319	15.6	499	10 US-09-735-169A-2	Sequence 2, Appl1
30	319	15.6	499	10 US-09-735-171A-2	Sequence 2, Appl1
31	295.5	14.5	313	9 US-10-121-746-81	Sequence 81, Appl1
32	295.5	14.5	313	10 US-09-735-169A-8	Sequence 8, Appl1
33	295.5	14.5	313	10 US-09-735-171A-8	Sequence 8, Appl1
34	294.5	14.4	332	10 US-09-735-169A-5	Sequence 5, Appl1
35	294.5	14.4	332	10 US-09-735-171A-5	Sequence 5, Appl1
36	190.5	9.3	383	10 US-09-939-484-7	Sequence 7, Appl1
37	190.5	9.3	383	10 US-09-939-483-7	Sequence 7, Appl1
38	179	8.8	39	10 US-09-746-491-63	Sequence 63, Appl1
39	176.5	8.6	107	10 US-09-828-746-4	Sequence 4, Appl1
40	156	7.6	347	10 US-09-939-483-6	Sequence 6, Appl1
41	156	7.6	347	10 US-09-939-483-6	Sequence 6, Appl1
42	131.5	6.4	646	9 US-10-121-746-10	Sequence 10, Appl1
43	123.5	6.0	223	9 US-09-875-321-9	Sequence 9, Appl1
44	123.5	6.0	223	9 US-10-162-012-9	Sequence 9, Appl1
45	118	5.8	988	9 US-09-875-321-12	Sequence 12, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-939-484-4  
Sequence 4, Application US/09939484  
Patent No. US20020032322A1  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Fink, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
FILE REFERENCE: 1201-CIP-DIV-00  
CURRENT APPLICATION NUMBER: US/09/939,484  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/144,914  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 08/749,816  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/095,234  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: FR 96/01565  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TASK  
US-09-939-484-4  
Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 MKRONVRLTALIVCTFTYLLGCAVFDLSEPELIERQRLERLQOELRARNYSOGYE 60  
DB 1 MKRONVRLTALIVCTFTYLLGCAVFDLSEPELIERQRLERLQOELRARNYSOGYE 60  
CY 61 ELERVLRLKHKKGVCGRFAGSEYFATVTTTGYGHAAPSTGCKVCFYALIGPL 120  
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Db 61 ELERVVLRLLKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGKRVCFMRYALLGIPL 120  
QY 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
Db 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
Db 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 2

US-09-939-483-4  
Sequence 4, Application US/09939483  
Patent No. US20020094558A1  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Fluk, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
FILE REFERENCE: 1201-CIP-DIV-2-00  
CURRENT APPLICATION NUMBER: US/09/939,483  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/144,914  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 08/749,816  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/095,234  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: FR 96/01565  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 4  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TASK  
US-09-939-483-4

Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLTALVCTFTYLLVGAAVDALESEBELERORLELROELRARNVLSGGYE 60  
Db 1 MKRONVRLTALVCTFTYLLVGAAVDALESEBELERORLELROELRARNVLSGGYE 60  
QY 61 ELERVVLRLLKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGKRVCFMRYALLGIPL 120  
Db 61 ELERVVLRLLKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGKRVCFMRYALLGIPL 120  
QY 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
Db 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240

Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
Db 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 3

US-09-798-584-15  
Sequence 15, Application US/09798584  
Patent No. US20020102676A1  
GENERAL INFORMATION:  
APPLICANT: Mu, David  
APPLICANT: Powers, Scott  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: KCNB: A NO. US20020102676A1 Potassium Channel Protein  
FILE REFERENCE: 018781-004010US  
CURRENT APPLICATION NUMBER: US/09/798,584  
CURRENT FILING DATE: 2001-03-03  
PRIOR APPLICATION NUMBER: US 60/186,951  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 394  
TYPE: PRT  
ORGANISM: human  
FEATURE:  
OTHER INFORMATION: human potassium channel KCNK3 (TASK1)  
US-09-798-584-15

Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLTALVCTFTYLLVGAAVDALESEBELERORLELROELRARNVLSGGYE 60  
Db 1 MKRONVRLTALVCTFTYLLVGAAVDALESEBELERORLELROELRARNVLSGGYE 60  
QY 61 ELERVVLRLLKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGKRVCFMRYALLGIPL 120  
Db 61 ELERVVLRLLKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGKRVCFMRYALLGIPL 120  
QY 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
Db 121 TLVMPFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALQKDALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
Db 241 LVVLRMTNMAEDKDAEHRALLTRNGAGGGGGSAAHTTDTASTAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCLMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 4

```

US-09-939-484-5
; Sequence 5, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-5

```

```

Query Match      89.1%; Score 1819; DB 10; Length 405;
Best Local Similarity 88.1%; Pred. No. 1,4e-161;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVTLLIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYELE 63
   1 ENVTLLIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYELE 60
DB 1
QY 64 RVLRLKPKHAGVQWRAGSFYFAITVITTYIGHAPSTDGKVFPCMFALLGIPLTIV 123
   61 RVLRLKPKHAGVQWRAGSFYFAITVITTYIGHAPSTDGKVFPCMFALLGIPLTIV 120
DB 1
QY 124 MFSLSGERINTVLYLLHRAKKGIGMRADYMANVYLIGFSCISTLCIGAAAFSHYEH 183
   121 MFSLSGERINTVLYLLHRAKKGIGMRADYMANVYLIGFSCISTLCIGAAAFSHYEH 180
DB 1
QY 184 WTEFOAYYYCFITLTITGFGDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 243
   181 WTEFOAYYYCFITLTITGFGDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 240
DB 1
QY 244 LRFWTMAEDKDAEHRALLTRNGOAGGGG-----GSAHTTDTASTAA----- 291
   241 LRFWTMAEDKDAEHRALLTRNGOAGGGG-----GSAHTTDTASTAA----- 291
DB 1
QY 292 --GGGCFRNYAAYLVHFOQSMCCLMYKSRKLOYSIPMIIPROLDSTSDTCVEOSHSSPGG 349
   301 GVGSGFRNYAAYLVHFOQSMCCLMYKSRKLOYSIPMIIPROLDSTSDTCVEOSHSSPGG 360
DB 1
QY 350 GGRYSPTPSRRCLCSGAPRSATSSVTGLHSLSTFRGLMKRRSSV 394
   361 GGRYSPTPSRRCLCSGAPRSATSSVTGLHSLSTFRGLMKRRSSV 405
DB 1

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RESULT 5
US-09-939-483-5
; Sequence 5, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel

```

```

; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-5

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Query Match      89.1%; Score 1819; DB 10; Length 405;
Best Local Similarity 88.1%; Pred. No. 1,4e-161;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVTLLIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYELE 63
   1 ENVTLLIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYELE 60
DB 1
QY 64 RVLRLKPKHAGVQWRAGSFYFAITVITTYIGHAPSTDGKVFPCMFALLGIPLTIV 123
   61 RVLRLKPKHAGVQWRAGSFYFAITVITTYIGHAPSTDGKVFPCMFALLGIPLTIV 120
DB 1
QY 124 MFSLSGERINTVLYLLHRAKKGIGMRADYMANVYLIGFSCISTLCIGAAAFSHYEH 183
   121 MFSLSGERINTVLYLLHRAKKGIGMRADYMANVYLIGFSCISTLCIGAAAFSHYEH 180
DB 1
QY 184 WTEFOAYYYCFITLTITGFGDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 243
   181 WTEFOAYYYCFITLTITGFGDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 240
DB 1
QY 244 LRFWTMAEDKDAEHRALLTRNGOAGGGG-----GSAHTTDTASTAA----- 291
   241 LRFWTMAEDKDAEHRALLTRNGOAGGGG-----GSAHTTDTASTAA----- 291
DB 1
QY 292 --GGGCFRNYAAYLVHFOQSMCCLMYKSRKLOYSIPMIIPROLDSTSDTCVEOSHSSPGG 349
   301 GVGSGFRNYAAYLVHFOQSMCCLMYKSRKLOYSIPMIIPROLDSTSDTCVEOSHSSPGG 360
DB 1
QY 350 GGRYSPTPSRRCLCSGAPRSATSSVTGLHSLSTFRGLMKRRSSV 394
   361 GGRYSPTPSRRCLCSGAPRSATSSVTGLHSLSTFRGLMKRRSSV 405
DB 1

```

```

RESULT 6
US-09-746-491-61
; Sequence 61, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: NO. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61
; LENGTH: 258
; TYPE: PRT

```

ORGANISM: Mus musculus  
US-09-746-491-61

Query Match Best Local Similarity 96.1%; Score 1278; DB 10; Length 258;  
Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
QY 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
DB 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
QY 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
DB 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258

## RESULT 7

US-09-798-584-1  
Sequence 1, Application US/09798584  
Patent No. US20020102676a1

GENERAL INFORMATION:  
APPLICANT: Mu, David  
APPLICANT: Powers, Scott  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: KCNB: A No. US20020102676a1el Potassium Channel Protein  
FILE REFERENCE: 018781-00401005  
CURRENT APPLICATION NUMBER: US/09/798,584  
CURRENT FILING DATE: 2001-03-03  
PRIOR APPLICATION NUMBER: US 60/186,951  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)  
US-09-798-584-1

Query Match Best Local Similarity 54.7%; Score 1116; DB 10; Length 374;  
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
QY 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
DB 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
QY 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
DB 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258

DB 241 LVVLRMTNMADEKRD 258  
QY 301 AEVLHQSQCWLKYSREKLOYSIPMLIPRLSDTCVBOSSHSPGGGRYSDPSSR 359  
DB 287 KADVPDQVSCVCTCRSD--YGRSVAPQSFSAKLAPHYHSHISYIEEISPTLK 343  
QY 360 RCLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394  
DB 344 NSLFP---SPISISPGHLSFTDQRLMKRRSSV 374

## RESULT 8

US-09-746-491-60  
Sequence 60, Application US/09746491  
Patent No. US20020137202A1

GENERAL INFORMATION:  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-621  
CURRENT APPLICATION NUMBER: US/09/746,491  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: USSN 60/171,329  
PRIOR FILING DATE: 1999-12-21  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 60  
LENGTH: 365  
TYPE: PRT  
ORGANISM: Cavia porcellus  
US-09-746-491-60

Query Match Best Local Similarity 52.4%; Score 1069.5; DB 10; Length 365;  
Matches 226; Conservative 43; Mismatches 94; Indels 33; Gaps 6;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEBELIERORLELROQELRARVNLISOGYE 60  
QY 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
DB 61 ELERVVLRLKPKHAGVQVMPAGSFYPAITVITTTIGGHAAPSTDGKRVCFMFAALLGIP 120  
QY 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPFSLGERINTLVRYLLHRAKKGIGMRADVSNANVLTIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
DB 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQTOPQVAFSEFYIITGLTVIGAFNL 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258  
QY 299 VVAEVLHQSQCWLKYSREKLOYSIPMLIPRLSDTCVBOSSHSPGGGRYSDPSSR 358  
DB 292 -----DLQSVSCACACYSRSP--QNGGATLAPPLHSHISCRLEI-----SPS 331  
QY 359 RCLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394  
DB 332 --TLKNSLFPSPISVSPGLHSGDNDHRLMLRRKS 365

## RESULT 9

US-09-746-491-59  
Sequence 59, Application US/09746491  
Patent No. US20020137202A1

GENERAL INFORMATION:  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-621

	Query Match	41.0%;	Score 838;	DB 10;	Length 330;
	Best Local Similarity	64.3%;	Pred. No. 4.3e-70;		
	Matches	166;	Conservative	32;	Mismatches 60; Indels 0; Gaps 0;
OY	1	MKRONVETLALIVCTFTYLLVGAAVPDLASEPELIEORLELROQELRARYNLSOGYE	60		
Db	1	MRRPSVRAGVLVCTLCYLGVGAVPDLASESGRQLLRGALRRRFGEFAEDYR	60		
OY	61	ELENVNLRLKHAKGVOMRFGASYFAITVTITTTGYGHADSTDGKVFECFAYALLGPL	120		
Db	61	ELERLALQAEHRARGROMKFEGSEFYFAITVTITTTIEYGHAAGTDSGKVFECFAYALLGPL	120		
OY	121	TLVAFOSIGEBINTLVRLHLRAKKGGMRADYSMANMNVLTGFSCSLSTICIGNAASH	180		
Db	121	TLTVFOSIGEBLNVAVRRLTLAAACCGILRTVCSTENLVVAGGLACCAATLALGNVASH	180		

RESULT 12  
 US-09-864-761-34389  
 : Sequence 34389, Application US/09864761  
 : Patent No. US20020048763A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Penn, Sharron G.  
 : APPLICANT: Rank, David R.  
 : APPLICANT: Hanzel, David K.  
 : APPLICANT: Chen, Weisheng  
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 : TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 : FILE REFERENCE: Aecmclxa X-1  
 : CURRENT APPLICATION NUMBER: US/09/864,761  
 : CURRENT FILING DATE: 2001-05-23





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: APPLICANT: Lesage, Florian
: APPLICANT: Fink, Michel
: APPLICANT: Lazdunski, Michel
: TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
: FILE REFERENCE: 1201-CIP-DIV-2-00
: CURRENT APPLICATION NUMBER: US/09/939,483
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: 09/144,914
: PRIOR FILING DATE: 1998-09-01
: PRIOR APPLICATION NUMBER: 08/749,816
: PRIOR FILING DATE: 1996-11-15
: PRIOR APPLICATION NUMBER: 60/095,234
: PRIOR FILING DATE: 1998-08-04
: PRIOR APPLICATION NUMBER: FR 96/01565
: PRIOR FILING DATE: 1996-02-08
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO: 8
: LENGTH: 370
: TYPE: PRT
: ORGANISM: Murine
: FEATURE:
: OTHER INFORMATION: TREK-1
: US-09-939-483-8

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Query Match      18.1%; Score 370; DB 10; Length 370;
Best Local Similarity 31.6%; Pred. No. 2.5e-26;
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

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Qy 1 MKRONVRLALIVCTFTYLLVGAANFDALSEPELIERORLELNOELRARNYNSQSGYE 60
Db 42 MKKRTVSTIFLVV--VYLIIGAANFKALEPOEISQRTTIVIOKOTFIADHACVNS--T 97
Qy 61 ELERNVRL-KPHKAGV-----QWRFAGSFYFAITVITTTIGYGHAPSTGGKV 108
Db 98 ELDELIOQIVAINAGIIPLGSSNOVSHMDLGSSFFAGVITTTIGYGHAPSTGGKI 157
Qy 109 FCMFYALLGIPLLTVMFQSLGERINTLVRYLLHRAKKGGMRRAD-----VSM 156
Db 158 FCIYIALLGIPLLFGLAGVGDQGTIF-----GKGIAKVEDTFIKWNVGQTKIRI 208
Qy 157 ANMYLIGFSCISTLCIGAAAFSHYEHMTFFQAYYCCITLTITGFGDYVALOKDQALOT 216
Db 209 ISTIIFLFGCVLVALPAVIFKHIEGMSALDAIFYVITLTITGFGDYVAGSD--LEY 266
Qy 217 QPOYVAFSEVYIITGLTVIGAFNLV--VLRFTMNADEKRD--AEHRALLTRN 267
Db 267 LDFYKPVVWFILVGLAFVAFVLSMIGDMLRVISKTKTEEVGEFFRAHAAEWNTAN 320

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RESULT 15
US-09-828-746-6
: Sequence 6, Application US/09828746
: Patent No. US20020028485A1
: GENERAL INFORMATION:
: APPLICANT: Helen Jane Meadows
: APPLICANT: Conrad Gerald Chapman
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30031-D1
: CURRENT APPLICATION NUMBER: US/09/828,746
: CURRENT FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: US 09/236,080
: PRIOR FILING DATE: 1999-01-25
: PRIOR APPLICATION NUMBER: EP 98300570.3
: PRIOR FILING DATE: 1998-01-27
: PRIOR APPLICATION NUMBER: UK 9822135.1
: PRIOR FILING DATE: 1998-10-09
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 6
: LENGTH: 411
: TYPE: PRT

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: ORGANISM: HOMO SAPIENS
: US-09-828-746-6

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Query Match      18.1%; Score 369; DB 10; Length 411;
Best Local Similarity 31.6%; Pred. No. 3.6e-26;
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

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Qy 1 MKRONVRLALIVCTFTYLLVGAANFDALSEPELIERORLELNOELRARNYNSQSGYE 60
Db 42 MKKRTVSTIFLVV--VYLIIGAANFKALEPOEISQRTTIVIOKOTFIADHACVNS--T 97
Qy 61 ELERNVRL-KPHKAGV-----QWRFAGSFYFAITVITTTIGYGHAPSTGGKV 108
Db 98 ELDELIOQIVAINAGIIPLGSSNOVSHMDLGSSFFAGVITTTIGYGHAPSTGGKI 157
Qy 109 FCMFYALLGIPLLTVMFQSLGERINTLVRYLLHRAKKGGMRRAD-----VSM 156
Db 158 FCIYIALLGIPLLFGLAGVGDQGTIF-----GKGIAKVEDTFIKWNVGQTKIRI 208
Qy 157 ANMYLIGFSCISTLCIGAAAFSHYEHMTFFQAYYCCITLTITGFGDYVALOKDQALOT 216
Db 209 ISTIIFLFGCVLVALPAVIFKHIEGMSALDAIFYVITLTITGFGDYVAGSD--LEY 266
Qy 217 QPOYVAFSEVYIITGLTVIGAFNLV--VLRFTMNADEKRD--AEHRALLTRN 267
Db 267 LDFYKPVVWFILVGLAFVAFVLSMIGDMLRVISKTKTEEVGEFFRAHAAEWNTAN 320

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Job time : 27 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 15:11:12 : Search time 72 Seconds

(Without alignments)  
729.177 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042  
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2042	100.0	394	AAV79674	Human potassium ch
3	2042	100.0	394	AAV87291	Human signal pepti
4	1819	89.1	405	AAV95230	Mouse potassium ch
5	1235.5	60.5	309	AAU07620	Mouse 2p channel p
6	1116	54.7	374	AAAB18807	Amino acid sequenc
7	1116	54.7	374	AAAB18813	Protein encoded by
8	1116	54.7	374	AAAG63958	Amino acid sequenc
9	1116	54.7	374	AAE22969	Human TWIK-9 prote
10	1116	54.7	374	AAE13279	Human transporters

11	846	41.4	400	22	AAE10679	Human TWIK-6 (G 16
12	838	41.0	330	22	AAAB47334	FCTR1 Homo sapi
13	838	41.0	400	22	AAE10678	Human TWIK-6 (E 16
14	838	41.0	400	23	AAE13286	Human transporters
15	785.5	38.5	436	22	ABG29273	Novel human diageno
16	777	38.1	340	22	ABB64375	Drosophila melanog
17	774	37.9	279	22	ABB28454	Peptide #1105 enco
18	774	37.9	279	22	ABB33636	Peptide #1142 enco
19	774	37.9	279	22	ABBI9091	Protein #1090 enco
20	774	37.9	279	22	AAAB4409	Human brain expres
21	774	37.9	279	22	AAAB6810	Human bone marrow
22	774	37.9	279	22	AAAI4676	Peptide #1110 enco
23	774	37.9	279	22	AAAB7095	Peptide #1132 enco
24	774	37.9	279	22	AAAB2399	Peptide #1081 enco
25	774	37.9	279	22	ABG36465	Human peptide enco
26	773	37.9	408	22	AAAB1804	Amino acid sequenc
27	742	36.3	398	22	ABAB7187	Drosophila melanog
28	379	18.6	361	22	AAAB1805	Amino acid sequenc
29	370	18.1	411	21	AAE10342	Murine TREK-1 pota
30	369	18.1	370	20	AAV30648	A mechanically sen
31	369	18.1	411	20	AAV28497	Mouse h-TREK1 poly
32	366.5	17.9	295	23	AAE21164	Human TRIC-8 prot
33	364	17.8	426	22	AAU07618	Human potassium io
34	363	17.8	411	20	AAV34133	Human potassium ch
35	363	17.8	411	20	AAV28496	h-TREK1 polypeptid
36	363	17.8	411	21	AAE10341	Human TREK-1 potas
37	363	17.8	411	22	AAAB5044	Human TREK. Homo
38	362	17.7	292	23	AAV09893	Rat potassium chan
39	362	17.7	292	23	AAV09894	Mouse potassium ch
40	361	17.7	292	23	AAV09892	Human potassium ch
41	360	17.6	426	22	AAU07622	Human potassium io
42	359	17.6	426	22	AAU07623	Human potassium io
43	358	17.5	534	23	AAU01355	Novel human ion ch
44	356	17.4	426	22	AAU07625	Human potassium io
45	355	17.4	411	23	AAE16597	Human TWIK-Related

#### ALIGNMENTS

RESULT 1  
AAE10343  
ID AAE10343 standard; Protein: 394 AA.  
AC AAE10343;  
XX 10-DEC-2001 (first entry)  
XX Murine TASK potassium channel protein.  
XX Murine TASK potassium channel protein.  
XX Murine: potassium channel protein; TREK-1; TASK; anaesthetic; analgesia;  
XX amnesia.  
XX Mus sp.  
XX WO200047738-A2.  
XX 17-AUG-2000.  
XX 11-FEB-2000; 2000WO-IB00226.  
XX 12-FEB-1999; 99US-0119727.  
XX 11-FEB-2000; 2000US-0503069.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
XX WPL: 2000-549146/50.  
XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
XX transfecting cells to be used to identify compounds with anesthetic  
XX properties -

XX Claim 23: Page 34-35; 39pp; English.

PS The invention relates to human and mouse TREK-1 potassium channel

XX proteins and their corresponding DNA molecules. TREK-1 nucleic acid is

CC useful for transfecting cells to induce expression of the TREK-1

CC potassium channel protein. These cells are then used in assays to

CC identify compounds which have anaesthetic properties, producing a safe,

CC reversible state of unconsciousness with concurrent amnesia and analgesia

CC in a mammal upon inhalation. The present sequence is murine TASK

CC potassium channel protein related to the invention.

XX

SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

Best Local Similarity 100.0%; Pred. No. 7.8e-214;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYE 60

DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYE 60

QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAPSTDGKVFQCMFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAPSTDGKVFQCMFYALLGIP 120

QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANNAVYLIGFSCISTLCIGAAAFSH 180

DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANNAVYLIGFSCISTLCIGAAAFSH 180

QY 181 YEHWTFQAYVYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

DB 181 YEHWTFQAYVYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

QY 241 LVVLRMTNNAEDEKDAEHRALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

DB 241 LVVLRMTNNAEDEKDAEHRALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

QY 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

DB 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

QY 361 CLOSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 CLOSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2

AAV79674

ID AAV79674 standard; Protein; 394 AA.

XX

AC AAV79674;

XX

DT 29-AUG-2000 (first entry)

XX

DE Human potassium channel TASK1.

XX

KW TASK1: TWIK-related acid-sensitive K+ channel 1; human;

KW potassium channel; drug screening; hypertension;

KW hypotensive; epilepsy; arrhythmia; vascular diseases;

KW neurodegenerative disease; ischemia; anoxia; endocrine disease;

KW muscle disease; therapy.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Modified-site 53

FT Modified-site /note- "N-glycosylated"

FT Modified-site 323

FT Modified-site /note- "O-phosphorylated"

FT Modified-site 383

FT Modified-site /note- "O-phosphorylated"

FT Modified-site 392

FT /note- "O-phosphorylated"

FT Modified-site 393

FT /note- "O-phosphorylated"

XX

XX W0200027871-A2.

XX

XX 18-MAY-2000.

XX

XX 09-NOV-1999; 99NO-IB01886.

XX

XX 09-NOV-1998; 98US-0107692.

XX

XX 08-NOV-1999; 99US-0436265.

XX

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX

XX Duprat F, Lesage F, Lazdunski M;

XX

XX WPI, 2000-376487/32.

XX

XX N-PSDB; AAA27746.

DR

DR New nucleic acid encoding a non-inactivating outwardly rectifying

PT potassium transport channel, designated TASK2, useful in the treatment

PT of hypertension or dysfunctions of the kidney, liver or pancreas -

PS disclosure; Fig 8; 91pp; English.

XX

XX The present sequence is that of human TASK1 (TWIK-related

CC acid-sensitive K+ channel), a member of a new family of 2P

CC domain potassium channels, also including TWIK-1 (see AAV79673) and

CC novel TASK2 (see AAV79675). TASK1 is expressed in many different

CC tissues, and at particularly high levels in pancreas and placenta.

CC Host cells expressing TWIK-1 family members can be used to screen

CC for substances that modulate the activity of members of the TWIK-1

CC family of potassium channels. The drugs identified may be

CC useful in the treatment of diseases of the heart or of the nervous

CC system, such as epilepsy, arrhythmia, vascular diseases,

CC neurodegenerative diseases, kidney, liver or pancreas diseases,

CC hypertension, diseases associated with ischemia or anoxia,

CC endocrine diseases associated with anomalies of hormone secretion,

CC and muscle diseases.

XX

XX

SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

Best Local Similarity 100.0%; Pred. No. 7.8e-214;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYE 60

DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROELRARNYLSGGYE 60

QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAPSTDGKVFQCMFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAPSTDGKVFQCMFYALLGIP 120

QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANNAVYLIGFSCISTLCIGAAAFSH 180

DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANNAVYLIGFSCISTLCIGAAAFSH 180

QY 181 YEHWTFQAYVYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

DB 181 YEHWTFQAYVYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

QY 241 LVVLRMTNNAEDEKDAEHRALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

DB 241 LVVLRMTNNAEDEKDAEHRALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

QY 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

DB 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

QY 361 CLOSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 CLCSGAPRSAISSVTGLHSLSTFRGLMKRRSSV 394

RESULT 3  
AAV87291  
ID AAV87291 standard; Protein: 394 AA.  
XX  
AC AAV87291;  
XX  
DT 11-MAY-2000 (first entry)  
XX  
DE Human signal peptide containing protein HSP68 SEQ ID NO:68.  
XX  
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW anti-infective; neuroprotective; cardiovascular; hepatocytic;  
KW antidiabetic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cleftosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's disease; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN MO200000610-A2.  
XX  
PD 06-JAN-2000.  
XX  
PE 25-JUN-1999; 99WO-US14484.  
XX  
PR 26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
XX  
XX  
PA (INCY-) INCYTE PHARM INC.  
PI Lal P. Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
XX  
DR WPI: 2000-160673/14.  
DR N-PSDB: AAZ98176.  
XX  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
XX  
PS (claim 1; Page 207-208; 327pp; English.  
XX  
CC AA298109 to AA298242 encode AAV87224 to AAV87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antidiabetic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cleftosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring). In gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
XX  
SO Sequence 394 AA;  
XX  
Query Match 100.0%; Score 2042; DB 21; Length 394;  
Best Local Similarity 100.0%; Pred. No. 7.8e-214;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKRONVRLALIVCTFFYLVLGAAPDALESEPELIERORLELROQLRARNYLSOGYE 60  
DB 1 MKRONVRLALIVCTFFYLVLGAAPDALESEPELIERORLELROQLRARNYLSOGYE 60  
QY 61 ELEHVYLRKPKHAKGVOMRFGSFYFAITVTTTGYHAPSTGKVFYALLGIPL 120  
DB 61 ELEHVYLRKPKHAKGVOMRFGSFYFAITVTTTGYHAPSTGKVFYALLGIPL 120  
QY 121 TLVVFOSIGERINTLVRLHRAKKGGMRAVDYMANMYLIGFSCISTICGAAAFSH 180  
DB 121 TLVVFOSIGERINTLVRLHRAKKGGMRAVDYMANMYLIGFSCISTICGAAAFSH 180  
QY 181 YEHWTFQAYVYCEITLTITIGFDYVALQKDOALQTOPOVYAFSVYILTGLTYIGAFLN 240  
DB 181 YEHWTFQAYVYCEITLTITIGFDYVALQKDOALQTOPOVYAFSVYILTGLTYIGAFLN 240  
QY 241 LVYLRFTMTNADKRDRAEHRALLTRNGQAGGGGSAHTTDPASTAAGGCFRNVY 300  
DB 241 LVYLRFTMTNADKRDRAEHRALLTRNGQAGGGGSAHTTDPASTAAGGCFRNVY 300  
QY 301 AEVLHFOGMCCLWYKSKREKQYSIPMTIPRDLSTSDTCVQSHSPGCGGRYSDDPSRR 360  
DB 301 AEVLHFOGMCCLWYKSKREKQYSIPMTIPRDLSTSDTCVQSHSPGCGGRYSDDPSRR 360  
QY 361 CLCSGAPRSAISSVTGLHSLSTFRGLMKRRSSV 394  
DB 361 CLCSGAPRSAISSVTGLHSLSTFRGLMKRRSSV 394

RESULT 4  
AAV95230  
ID AAV95230 standard; Protein: 405 AA.  
XX  
XX  
AC AAV95230;  
XX  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Mouse potassium channel TASK.  
XX  
XX  
KW TASK: TWIK-related acid-sensitive K<sup>+</sup> channel; mouse;  
KW potassium channel; drug screening; hypertension;  
KW hypotensive; epilepsy; arrhythmia; vascular diseases;  
KW neurodegenerative disease; ischaemia; anoxia; endocrine disease;  
KW muscle disease; therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 50  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 334  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 403  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 404  
FT Modified-site /note= "O-phosphorylated"  
XX  
PN MO200027871-A2.  
XX  
PD 18-MAY-2000.  
XX  
XX  
PF 09-NOV-1999; 99WO-IB01886.  
XX  
XX  
PR 09-NOV-1998; 98US-0107692.

PR	08-NOV-1999;	99US-0436265.
XX	(CNRS ) CNRS CENT NAT RECH SCI.	
PA	Duprat F, Lesage F, Lazdunski M:	
PI	WPI; 2000-376487/32.	
XX		
DR	New nucleic acid encoding a non-inactivating outwardly rectifying	
PT	potassium transport channel, designated TASK2, useful in the treatment	
PT	of hypertension or dysfunctions of the kidney, liver or pancreas -	
XX		
PS	Disclosure; Fig 8; 91pp; English.	
XX		
CC	The present sequence is that of murine TASK (TWIK-related	
CC	acid-sensitive K <sup>+</sup> channel), a member of a new family of 2p	
CC	domain potassium channels, also including human TWIK-1 (see	
CC	AA179673), human TASK1 (see AA179674) and novel human TASK2 (see	
CC	AA179675). Human and mouse TASK proteins share 85% identity,	
CC	indicating that they are products of orthologue genes. Host	
CC	cells expressing TWIK-1 family members can be used to screen	
CC	for substances that modulate the activity of members of the TWIK-1	
CC	family of potassium channels. The drugs identified may be	
CC	useful in the treatment of diseases of the heart or of the nervous	
CC	system, such as epilepsy, arrhythmia, vascular diseases,	
CC	neurodegenerative diseases, kidney, liver or pancreas diseases,	
CC	hypertension, diseases associated with ischemia or anoxia,	
CC	endocrine diseases associated with anomalies of hormone secretion,	
CC	and muscle diseases.	
SO	Sequence 405 AA:	
	Query Match 89.1%; Score 1819; DB 21; Length 405;	
	Best Local Similarity 88.1%; Pred. No. 1.8e-189;	
	Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2	
OY	4 ONVRRLALIVCTFTYLVLGAAYFDLSEPELIERORLERODELRAKYNLSGGYEELT 63	
DB	1 ENVRLLALIVCTFTTLVLGAAYFDLSEPELIEROLELRLELRARINLSEGGYEELT 60	
OY	64 RVLRLKPKHKGAVOMRFAGSEFFAIVTYITIGYGHAPSTDGKYFCMEYALLGIPLTV 123	
DB	61 RVLLRKPKHKGAVQMRFGASFEFAIVTYITIGYGHAADSTDGKVFCEMYALLGIPLTI 120	
OY	124 MFQSIGEIRINTLVRLILRRARKGLGRADYSMAMNVLGFSCISTLCIGAARSHYEH 183	
DB	121 MFQSGEIRINFVRYLLRPARKGLGMRIAEVSMMANVNLGFVSCISTLCIGAARSYYER 180	
OY	184 WTFPGAYYYCFTLTITIGFCDVALOKKOALOTOPQYAFSVYLIITGLTVGAFLNLVY 243	
DB	181 WTFPGAYYYCFITLTITIGFCDVALOKKOALOTOPQYAFSVYLIITGLTVGATLNLY 240	
OY	244 LRFMTMAEDEKRDAENRALLTRNGOAGGGG-----GGSANTTDASTAA-- 291	
DB	241 LRFMTMAEDEKRDAENRALLTRNHQAAGLGSLCSLGSIGLGVRRDPDYTCAAAAGVG 300	
OY	292 --GGGGFENVYAELYHFQSMCSCLMYKSRKKLOYSIPMLIPRDLSPTDCVSHSSPQG 349	
DB	301 GVGSGGFENVYAELYHFQSMCSCLMYKSRKKLOYSIPMLIPRDLSPTCVHSHSSPQG 360	
OY	350 GGRVSDTPSRRCLSGADPASAISVSYTGLSHSIFSTRGLMKRRSSV 394	
DB	361 GGRVSDTPSHPCLCGTGRSAISSYSTGLHSLAARGLMKRRSSV 405	
RESULT 5		
AAU07620	AAU07620 standard; Protein: 309 AA.	
AC	AAU07620:	
XX	21-NOV-2001 (first entry)	

```

DE Mouse 2P channel protein #1.
XX Transmembrane potassium ion channel protein; inward potassium flux;
XX pest control; membrane potential; pesticide; antihelminthic; nematode;
XX insect; 2P channel; mouse.
XX Mus musculus.
XX WO200161006-A2.
XX
XX PD 23-AUG-2001.
XX
XX PE 14-FEB-2001; 2001WO-US04680.
XX
XX PR 15-FEB-2000; 2000US-0503849.
XX
XX PA (BADI ) BASF CORP.
XX
XX PI Pausch MH;
XX
XX DR WPI: 2001-536570/59.
XX
XX DR N-PSDB: AAS12179.
XX
XX
XX PT New polypeptide, a mutant potassium ion channel protein for improving
XX inward potassium flux under acidic conditions
XX
XX PS Example 18; Page 53; 131pp; English.
XX
XX CC The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a mouse 2P channel protein.
XX
XX SQ Sequence 309 AA;
XX
XX Query Match 60.5%; Score 1235.5; DB 22; Length 309;
XX Best Local Similarity 83.9%; Pred. No. 5.9e-126;
XX Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3
XX
OY 4 QNVRTALIVCTFTYLLVGAADFALSEPELIERORLELRQELRLARYNLISGGYELE 63
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13 ENVRTALIVCTFTYLLVGAADFALSEPEMIEHRIERLRLRLARYNLISGGYELE 72
OY 64 RVLRLAKRKAGVQWRFGSEFYATVTTTIGYGAAASTDGGKFCMFYALLGIPRLV 123
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 RVLRLAKRKAGVQWRFGSEFYATVTTTIGYGAAASTDGGKFCMFYALLGIPRLV 132
OY 124 MFOSLGERINTLVRLTLHRAKKGLMRADYSMMANVTLIGFSCISTCIGAAAFSHEH 183
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
133 MFOSLGERINTSVRLTLHRAKKGLMRADYSMMANVTLIGFSCISTCIGAAAFSHEH 192
OY 184 WTFFOAYYTCITTTTIGFGDVALQKQALQTOPQYVAFSEFVITLGLTYIG--AFLNL 241
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 WTFFOAYYTCITTTTIGFGDVALQKQALQTOPQYVAFSA---SCTSSRAHGHRFNL 249
OY 242 VVLEFPMNNADEKRDADHRLALLRNGAGGGC-----GGSAHTTDPAASTPAA 291
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
250 VVLEFPMNNADEKRDADHRLALLRNGAGVGLSLGSGSLGDGVPRDPVTCAAA 307
XX
XX RESULT 6
XX ID AAB18807
XX AC AAB18807;
XX
XX ID AAB18807 standard; Protein: 374 AA.
XX
XX AC AAB18807;
XX

```

DT 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a human DKCN1 polypeptide.  
 DE  
 XX Human: DKCN1; potassium channel; cancer; pulmonary disease; depression;  
 KW cardiovascular disease; inflammatory disease; renal disease; pain;  
 KW psychiatric disorder; schizophrenia; neurodegenerative disease;  
 KW Alzheimer's disease; neurological disorder; migraine; epilepsy;  
 KW sleep-related disorder; erectile dysfunction; alopecia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200053628-A2.  
 XX  
 XX 14-SEP-2000.  
 XX  
 XX 02-MAR-2000; 2000WO-EP01750.  
 XX  
 XX 05-MAR-1999; 99GB-0005061.  
 PR 10-FEB-2000; 2000GB-0003112.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;  
 XX  
 XX WPI: 2000-587424/55.  
 DR N-PSDB: AAA75886.  
 XX  
 XX The present sequence represents human DKCN1 polypeptide. The polypeptide  
 CC is a member of the potassium channel family. The DKCN1 polypeptides and  
 CC polynucleotides are useful for treating diseases including cancer,  
 CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,  
 CC psychiatric disorders including depression and schizophrenia,  
 CC neurodegenerative disease including Alzheimer's, neurological disorders,  
 CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and  
 CC alopecia. DKCN1 polynucleotides are useful as diagnostic reagents for  
 CC detecting mutations in the associated gene.  
 CC  
 XX Sequence 374 AA:  
 SQ  
 Query Match 54.7%; Score 1116; DB 21; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-113;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERQRLRQELRARNYNSGGYE 60  
 DB 1 MKRONVRLSLIVCTFTYLLVGAADFALSDHEEREKKAERIRIKGYNTISSEDR 60  
 QY 61 ELERVVLRLKPKHKGAVQWRFGSFYFATVTTTIGYGAASSTGKVCFCFVALGTLPL 120  
 DB 61 QLELVITLQSEPHRAGVQWKFAGSFYFATVTTTIGYGAAGTDAKGFACFVAVLGTLPL 120  
 QY 121 TLVNFOSLGERINTLVRYLRLHRAKGLGMRADVSMANMVLIGFSCSTICIGAAAFSH 180  
 DB 121 TLVNFOSLGERINTLVRYLRLKRIKCCGMRTDVMEMMYVGFSCMGTICIGAAAFSQ 180  
 QY 181 YEHTFPOAYYYCTITLTGFGDYVALQKDALQTOPQVYAFSFTVLTGLVYIGAFLN 240  
 DB 181 CEESFPHAYYYCTITLTGFGDYVALQKDALQKPLVYAFSFTVLTGLVYIGAFLN 240  
 QY 241 LVVLRFTMTNADEKRDARHALLTRNGAGGGGGCAHTTDAASSFAAGGGGFRNVY 300  
 DB 241 LVVLRFTMTNADEKRDARHALLTRNGAGGGGGCAHTTDAASSFAAGGGGFRNVY 300  
 QY 301 -AEVLHFOGSMCKMYKSRERLOYISIPMIIPRDLSTSDTCVEOSHSSPFGGGRYSDTPSPR 359  
 DB 301 -AEVLHFOGSMCKMYKSRERLOYISIPMIIPRDLSTSDTCVEOSHSSPFGGGRYSDTPSPR 359

DB 287 KADVPDLQSCVCTCYRSQD---YGRGSAVPQNSPAKLADHPHISIKIEISPSTLK 343  
 QY 360 RCLCSGAPRAISSVSTGLSLSTFRCLMKRRSSV 394  
 DB 344 NSLFP---SPISISSPGLSHSTPDHQRMLKRRKRV 374  
 RESULT 7  
 AAB18813  
 ID AAB18813 standard; Protein; 374 AA.  
 AC AAB18813;  
 XX  
 XX 22-JAN-2001 (first entry)  
 XX  
 XX Protein encoded by an EST related to a human DKCN1 cDNA.  
 DE  
 XX Human: DKCN1; potassium channel; cancer; pulmonary disease; depression;  
 KW cardiovascular disease; inflammatory disease; renal disease; pain;  
 KW psychiatric disorder; schizophrenia; neurodegenerative disease;  
 KW Alzheimer's disease; neurological disorder; migraine; epilepsy;  
 KW sleep-related disorder; erectile dysfunction; alopecia;  
 KW expressed sequence tag; EST.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO200053628-A2.  
 XX  
 XX 14-SEP-2000.  
 XX  
 XX 02-MAR-2000; 2000WO-EP01750.  
 XX  
 XX 05-MAR-1999; 99GB-0005061.  
 PR 10-FEB-2000; 2000GB-0003112.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;  
 XX  
 XX WPI: 2000-587424/55.  
 DR N-PSDB: AAA75887.  
 XX  
 XX The present sequence is encoded by an expressed sequence tag (EST) which  
 CC is related to a cDNA encoding a human DKCN1 polypeptide. The polypeptide  
 CC is a member of the potassium channel family. The DKCN1 polypeptides and  
 CC polynucleotides are useful for treating diseases including cancer,  
 CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,  
 CC psychiatric disorders including depression and schizophrenia,  
 CC neurodegenerative disease including Alzheimer's, neurological disorders,  
 CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and  
 CC alopecia. DKCN1 polynucleotides are useful as diagnostic reagents for  
 CC detecting mutations in the associated gene.  
 CC  
 XX Sequence 374 AA:  
 SQ  
 Query Match 54.7%; Score 1116; DB 21; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-113;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERQRLRQELRARNYNSGGYE 60  
 DB 1 MKRONVRLSLIVCTFTYLLVGAADFALSDHEEREKKAERIRIKGYNTISSEDR 60  
 QY 61 ELERVVLRLKPKHKGAVQWRFGSFYFATVTTTIGYGAASSTGKVCFCFVALGTLPL 120  
 DB 61 QLELVITLQSEPHRAGVQWKFAGSFYFATVTTTIGYGAAGTDAKGFACFVAVLGTLPL 120









PT activity -  
XX  
XX Claim 13; Fig 2; 123pp; English.

CC The present sequence is human TWIK-6 (G165) (' tandem of p domains in  
CC a weak inward rectifying K<sup>+</sup> channel) protein. TWIK-6 DNA and  
CC protein are useful for treating potassium channel-associated disorders,  
CC central nervous system (CNS) disorders (Parkinson's disease, Alzheimer's  
CC disease, dementia, Huntington's disease, senile dementia, Gilles de la  
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,  
CC progressive supranuclear palsy, epilepsy, Jakob-Creutzfeldt disease),  
CC autonomic function disorders (hypertension, sleep disorders, depression,  
CC neuropsychiatric disorders, schizophrenia, anxiety disorders,  
CC Korsakoff's psychosis, mania, phobic disorders), learning or memory  
CC disorders (amnesia, age-related memory loss, attention deficit disorder,  
CC dysrhythmic disorder, major depressive disorder, obsessive-compulsive  
CC disorder), psychosomatic substance use disorders, anxiety, phobias, panic  
CC disorder), bipolar affective disorder (migraine, obesity), cardiovascular  
CC system disorders (arteriosclerosis, ischaemia, reperfusion injury,  
CC restenosis, arterial inflammation, vascular wall remodelling, ventricular  
CC remodelling, rapid ventricular packing, coronary microembolism,  
CC tachycardia, bradycardia, pressure overload, aortic bending, coronary  
CC artery ligation, vascular heart disease, atrial fibrillation, Jervell  
CC syndrome, Lange-Nielsen syndrome, long-QT syndrome, congestive heart  
CC failure, sinus node dysfunction, angina, heart failure, hypertension,  
CC atrial fibrillation, atrial flutter, dilated cardiomyopathy, idiopathic  
CC cardiomyopathy, myocardial infarction, coronary artery disease and spasm,  
CC arrhythmias), musculoskeletal system disorders (paralysis, muscle weakness  
CC ataxia, myotonia and myokymia), cellular growth, differentiation or  
CC cell division disorders (cancer, carcinoma, sarcoma or leukaemia, tumour  
CC angiogenesis and metastasis, skeletal dysplasia, neuronal deficiencies  
CC resulting from impaired neural induction and patterning).  
CC neurodegenerative disorders, hepatic disorders, cardiovascular disorders  
CC and haematopoietic and/or myeloproliferative disorders. TWIK-6 DNA is  
CC useful in gene therapy.  
XX  
XX

Sequence 400 AA:

Query Match 41.4%; Score 846; DB 22; Length 400;  
Best Local Similarity 64.7%; Pred. No. 2.8e-83;  
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCFYLLVGAANFDALSEPELIEORLELROQELRARNYSOGYE 60  
DB 71 MRRPSVRAAGLVLTCLYLGAANFDALSEPELIEORLELROQELRARNYSOGYE 130  
QY 61 ELERVVLRLKPKHAGVQWRPAGSFYFALTIVTTIGYHAAPSTDGKVCMEFYALLGIPL 120  
DB 131 ELERLALQAEHPHRAGRQWKPFGSEFYFALTIVTTIGYHAAPSTDGKVCMEFYALLGIPL 190  
QY 121 TLVWFOSSGERTLTVRLRLRAKKGICMRADYSMMAMVLIQFSCSTLCIGAAASH 180  
DB 191 TLVWFOSSGERTLTVRLRLRAKKGICMRADYSMMAMVLIQFSCSTLCIGAAASH 250  
QY 181 YEHYTFQAYYYCFTLTLTIGFGDVALQKDAOTOPQYVAFSEFVYLTIGTVIGALIN 240  
DB 251 FEGWTFEAFYCYCFTLTLTIGFGDVALQKDAOTOPQYVAFSEFVYLTIGTVIGALIN 310  
QY 241 LVVLRFTMADEKRDRA 258  
DB 311 LVVLRFTMADEKRDRA 328

RESULT 12  
AAB47334 standard; Protein; 330 AA.  
XX  
XX AAB47334;  
XX  
XX 29-AUG-2001 (first entry)  
XX  
XX ECTRI1.  
XX

KW FCTR1; energy metabolism; adipose storage; muscle mass;  
KW insulin secretion; glucose utilization; serum lipid level;  
KW triglyceride; cholesterol; human; diabetes; metabolic disturbance;  
KW obesity; metabolic syndrome X; anorexia; infectious disease;  
KW cancer-associated cachexia; cancer; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidemia.

OS Homo sapiens.

FN Key Location/Qualifiers  
FN Peptide 1..23  
FT Protein /label= Signal peptide  
FT Protein 24..330  
FT Protein /label= Mature protein

XX WO200146231-A2.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US34898.

XX 21-DEC-1999; 99US-0171329.

XX 20-DEC-2000; 2000US-0171329.

XX (CURA-) CURAGEN CORP.

XX Burgess CE;

XX WPI; 2001-418026/44.

XX N-PSDB; AAC86163.

PT Novel FCTR1 polypeptides useful for treating, diagnosing and preventing  
PT diabetes, anorexia, obesity, cancer, neurodegenerative disorders,  
PT immune disorders and various lipidemias  
XX  
XX  
XX Claim 1; Page 31; 116pp; English.

CC This sequence shows a FCTR1 protein. The DNA sequence originates  
CC in chromosome 20. The FCTR1 protein is a novel K<sup>+</sup> channel-like  
CC protein and has a high probability of being sorted to the plasma  
CC membrane. The FCTR1 DNA was found to have 641 of 854 bases (75%),  
CC in a complete coding sequence of 2590 bases, identical to a human  
CC mRNA sequence encoding TWIK-related acid-sensitive K<sup>+</sup> channel (TASK).  
CC The FCTR1 protein has 168 of 258 residues (65%), identical to, and  
CC 200 of 258 residues (77%) positive with, mouse CTBAK having a total  
CC of 409 amino acids.

CC Note: This sequence is given as it is decoded from the corresponding  
CC DNA sequence. The specification includes additional amino acid  
CC sequences which are not encoded by the FCTR1 DNA.

CC FCTR1 polypeptides and associated nucleic acids are useful for  
CC treating or preventing a FCTR1-associated disorder related to  
CC energy metabolism in an organism that effects adipose stored, muscle  
CC mass, insulin secretion, glucose utilization and serum lipid levels  
CC including, triglycerides and cholesterol in human. These disorders  
CC include diabetes, metabolic disturbances associated with obesity,  
CC the metabolic syndrome X, anorexia, wasting disorders associated with  
CC chronic diseases, metabolic disorders, obesity, infectious disease,  
CC cancer-associated cachexia, cancer, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disorder, immune disorders,  
CC haematopoietic disorders, and various dyslipidemias.

XX Sequence 330 AA:

Query Match 41.0%; Score 838; DB 22; Length 330;  
Best Local Similarity 64.3%; Pred. No. 1.6e-82;  
Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCFYLLVGAANFDALSEPELIEORLELROQELRARNYSOGYE 60  
DB 1 MRRPSVRAAGLVLTCLYLGAANFDALSEPELIEORLELROQELRARNYSOGYE 120  
QY 61 ELERVVLRLKPKHAGVQWRPAGSFYFALTIVTTIGYHAAPSTDGKVCMEFYALLGIPL 120

```

Db 61 ELERLALQAEPRHAGQMKPGSEFYFAITVITTEIGHAAPGDSKVCMEFALLGIPL 120
Qy 121 TVMFQSLGERINTLVRYLLHRAKKGIMRADVSNANVYLIGFSCISTLTCGAAAFSH 180
Db 121 TVMTFQSLGERLNAVVRLLAAKCCIGRMTCVSTENLVAGLLCAATLALGAVAFSH 180
Qy 181 YEHMTFFQAYVYCFITLTITIGFDYVALQKDALQOPQVAVSFYITLGLTVIGAFIN 240
Db 181 FEGMTFFHAYVYCFITLTITIGFDYVALQSGEALQKRLPYVASFYITLGLTVIGAFIN 240
Qy 241 LVVLRFTMNAEDEKRD 258
Db 241 LVVLRFTVASADWPERAA 258

RESULT 13
AAE10678
ID AAE10678 standard; Protein; 400 AA.
XX
AC AAE10678;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human TWIK-6 (E 165) protein.
XX
KW Human: Tandem of P domains in a weak inward rectifying K+ channel-6;
KW TWIK-6; sensory nervous system disorder; cardiac; cellular proliferation;
KW haemopoietic; cytosolic; nocturnal; osteopathic; gene therapy; mania;
KW vacuole; potassium channel-associated disorder; Parkinson's disease;
KW Alzheimer's disease; dementia; Huntington's disease; multiple sclerosis;
KW amyotrophic lateral sclerosis; hypertension; depression; inflammation;
KW anxiety; amnesia; neuropsychiatric disorder; migraine; obesity; cancer;
KW arteriosclerosis; ischaemia; cardiomyopathy; myocardial infarction;
KW ataxia; arrhythmia; paralysis; muscle weakness; cellular growth; tumour;
KW carcinoma; leukaemia; hepatic disorder; gene therapy.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Domain 75..144
FT FT /note="TWIK-related ion channel domain"
FT FT 78..96
FT FT /label="Transmembrane_domain"
FT FT 81..312
FT FT /note="Potassium channel protein domain"
FT FT 150..166
FT FT /label="P-loop_domain"
FT FT /note="Pore-loop domain"
FT FT 178..195
FT FT /label="Transmembrane_domain"
FT FT 229..248
FT FT /label="Transmembrane_domain"
FT FT 260..278
FT FT /label="P-loop_domain"
FT FT /note="Pore-loop domain"
FT FT 290..314
FT FT /label="Transmembrane_domain"
XX
PN MO200166743-A2.
XX
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001MO-US06933.
XX
PR 03-MAR-2000; 2000US-0518866.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ, Glucksmann MA;
XX
DR WPI, 2001-596835/67.
DR N-PSDB; AAD17525.

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XX Novel TWIK-6 polypeptide of TWIK family of potassium channels for
PT treating sensory nervous system disorders, cardiac-related disorders
PT and cellular proliferation disorders comprises the modulation of its
PT activity -
PS Claim 13; Fig 1; 123pp; English.
XX
CC The present sequence is human TWIK-6 (E165) (Tandem of P domains
CC in a weak inward rectifying K+ channel) protein. TWIK-6 DNA and
CC protein are useful for treating potassium channel-associated disorders,
CC central nervous system (CNS) disorders (Parkinson's disease, Alzheimer's
CC disease, dementia, Huntington's disease, senile dementia, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC progressive supranuclear palsy, epilepsy, Jakob-Creutzfeldt disease),
CC autonomic function disorders (hypertension, sleep disorders, depression,
CC neuropsychiatric disorders, schizophrenia), learning or memory
CC disorders (amnesia, age-related memory loss, attention deficit disorder,
CC dysrhythmic disorder, major depressive disorder, obsessive-compulsive
CC disorder), bipolar affective disorder (mania, anxiety, phobias, panic
CC disorder), bipolar affective disorder (mania, anxiety, phobias, panic
CC system disorders (arteriosclerosis, ischaemia, reperfusion injury,
CC restenosis, arterial inflammation, vascular wall remodelling, ventricular
CC remodelling, rapid ventricular packing, coronary microembolism,
CC tachycardia, bradycardia, pressure overload, aortic bending, coronary
CC artery ligation, vascular heart disease, atrial fibrillation, coronary
CC syndrome, Lange-Nielsen syndrome, long QT syndrome, congestive heart
CC failure, sinus node dysfunction, angina, heart failure, hypertension,
CC atrial fibrillation, atrial flutter, dilated cardiomyopathy, idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease and spasm,
CC arhythmia), musculoskeletal system disorders (paralysis, muscle weakness
CC ataxia, myotonia and myofascia), cellular growth, differentiation or
CC migration disorders (cancer, carcinoma, sarcoma or leukaemia, tumour
CC angiogenesis and metastasis, skeletal dysplasia, neuronal deficiencies
CC resulting from impaired neural induction and patterning),
CC neurodegenerative disorders, hepatic disorders, cardiovascular disorders
CC and haematopoietic and/or myeloproliferative disorders. TWIK-6 DNA is
CC useful in gene therapy.
XX
SQ Sequence 400 AA;
Qy 1 MKRONRTALAVCYFTYLLVNGAAYDALESEBELERORLELRARVNLQSGYE 60
Db 71 MRRPSVRAAGLVCTCYLLVGAAYDPALESESGRRLVQKRGALRRKFGFSAEDR 130
Qy 61 ELERVVLRKPKHAGVQMRFGAGSFYFAITVITTEIGHAAPGDSKVCMEFALLGIPL 120
Db 131 ELERLALQAEPRHAGQMKPGSEFYFAITVITTEIGHAAPGDSKVCMEFALLGIPL 190
Qy 121 TVMFQSLGERINTLVRYLLHRAKKGIMRADVSNANVYLIGFSCISTLTCGAAAFSH 180
Db 191 TVMTFQSLGERLNAVVRLLAAKCCIGRMTCVSTENLVAGLLCAATLALGAVAFSH 250
Qy 181 YEHMTFFQAYVYCFITLTITIGFDYVALQKDALQOPQVAVSFYITLGLTVIGAFIN 240
Db 251 FEGMTFFHAYVYCFITLTITIGFDYVALQSGEALQKRLPYVASFYITLGLTVIGAFIN 310
Qy 241 LVVLRFTMNAEDEKRD 258
Db 311 LVVLRFTVASADWPERAA 328

RESULT 14
AAE13286
ID AAE13286 standard; Protein; 400 AA.
XX
AC AAE13286;
XX

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:18:47 ; Search time 27 Seconds

(without alignments)  
429.357 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued\_Patents\_AA: \*  
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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCtUS\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	US-09-144-914-4	Sequence 4, Appl1
2	1819	89.1	405	US-09-144-914-5	Sequence 5, Appl1
3	370	18.1	370	US-09-144-914-8	Sequence 8, Appl1
4	369	18.1	411	US-09-236-080-6	Sequence 6, Appl1
5	363	17.8	411	US-09-236-080-2	Sequence 2, Appl1
6	363	17.8	411	US-09-336-643A-83	Sequence 83, Appl1
7	329.5	16.1	393	US-09-432-470-2	Sequence 2, Appl1
8	329.5	16.1	393	US-09-432-470-4	Sequence 4, Appl1
9	320.5	15.7	336	US-08-749-816-2	Sequence 2, Appl1
10	320.5	15.7	336	US-09-144-914-2	Sequence 2, Appl1
11	295.5	14.5	313	US-09-336-643A-81	Sequence 81, Appl1
12	253	12.4	336	US-08-332-312-4	Sequence 4, Appl1
13	231.5	11.3	618	US-08-332-312-2	Sequence 2, Appl1
14	190.5	9.3	383	US-08-749-816-4	Sequence 4, Appl1
15	190.5	9.3	383	US-09-144-914-7	Sequence 7, Appl1
16	176.5	8.6	107	US-09-236-080-4	Sequence 4, Appl1
17	156	7.6	347	US-08-749-816-3	Sequence 3, Appl1
18	156	7.6	347	US-09-144-914-6	Sequence 6, Appl1
19	131.5	6.4	646	US-09-336-643A-10	Sequence 10, Appl1
20	113	5.5	197	US-09-336-643A-16	Sequence 16, Appl1
21	112.5	5.5	1082	US-09-336-643A-20	Sequence 20, Appl1
22	112.5	5.5	1082	US-09-600-776-2	Sequence 2, Appl1
23	112.5	5.5	1083	US-09-343-494-1	Sequence 1, Appl1
24	111.5	5.5	636	US-09-142-791A-2	Sequence 2, Appl1
25	111.5	5.5	636	US-09-178-109-4	Sequence 4, Appl1
26	111.5	5.5	655	US-09-142-791A-4	Sequence 4, Appl1
27	111.5	5.5	655	US-09-178-109-2	Sequence 2, Appl1

28	105.5	5.2	636	4	US-09-142-791A-6	Sequence 6, Appl1
29	103	5.0	532	1	US-08-288-405A-10	Sequence 10, Appl1
30	102.5	5.0	626	2	US-08-956-242-2	Sequence 2, Appl1
31	102.5	5.0	626	3	US-09-351-215-2	Sequence 2, Appl1
32	99.5	4.9	494	1	US-08-464-340A-4	Sequence 4, Appl1
33	99.5	4.9	494	5	PCT-US94-08449A-4	Sequence 4, Appl1
34	99.5	4.9	888	2	US-08-956-242-4	Sequence 4, Appl1
35	99.5	4.9	888	3	US-09-351-215-4	Sequence 4, Appl1
36	97.5	4.8	289	4	US-09-372-422A-14	Sequence 14, Appl1
37	97.5	4.8	1017	4	US-09-600-776-6	Sequence 6, Appl1
38	97	4.8	255	4	US-09-342-084-11	Sequence 11, Appl1
39	95.5	4.7	282	4	US-09-372-422A-8	Sequence 8, Appl1
40	95.5	4.7	288	4	US-09-372-422A-12	Sequence 12, Appl1
41	94	4.6	807	4	US-09-177-650-3	Sequence 3, Appl1
42	94	4.6	1159	2	US-08-956-242-13	Sequence 13, Appl1
43	94	4.6	1159	3	US-09-351-215-13	Sequence 13, Appl1
44	94	4.6	1159	4	US-09-226-012-2	Sequence 2, Appl1
45	94	4.6	1159	4	US-09-226-012-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-09-144-914-4

Sequence 4, Application US/09144914  
Patent No. 6309855

GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Lesage, Florian

APPLICANT: Fink, Michel

APPLICANT: Lazdunski, Michel

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS. THEIR CLONING

TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

FILE REFERENCE: 989.6705CIP

CURRENT FILING DATE: US/09/144.914

EARLIER FILING DATE: 1998-09-01

EARLIER FILING DATE: 1996-11-15

EARLIER FILING DATE: 1998-08-04

EARLIER APPLICATION NUMBER: 60/095,234

EARLIER FILING DATE: 1996-02-08

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 394

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: TASK

US-09-144-914-4

Query Match 100.0%; Score 2042; DB 4; Length 394;

Best Local Similarity 100.0%; Pred. No. 4.9e-218;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MKRQNVRLALIVCTFTYLLVGA	VDAL	SEPELIERORLE	ROELRARNLSOGYE	60
QY	61	ELERVVLTKPKHAGVORFAGS	FEAT	VTITTYGHAAPSTDG	KVFCMFYALGLPL	120
DB	61	ELERVVLTKPKHAGVORFAGS	FEAT	VTITTYGHAAPSTDG	KVFCMFYALGLPL	120
QY	121	TLVPOSIGERINTLVRLHRAK	KGLCMRADVSMAN	MYLIGFSCISTLCIGA	AAFSH	180
DB	121	TLVPOSIGERINTLVRLHRAK	KGLCMRADVSMAN	MYLIGFSCISTLCIGA	AAFSH	180
QY	181	YEHMTFFQAYYYCFTLTIT	TIGFGDYVALQKDAL	OTOPQYVAFSVYLLT	GLTVIGAFLN	240
DB	181	YEHMTFFQAYYYCFTLTIT	TIGFGDYVALQKDAL	OTOPQYVAFSVYLLT	GLTVIGAFLN	240





TYPE: PRT  
ORGANISM: Mus musculus  
US-09-236-080-6

Query Match 18.1%; Score 369; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 2.4e-32;  
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

OY 1 MKRONVRLALIVCFYLLVGAADFALSEPELIERORLELROOELRARNLSOGYE 60  
DB 42 MKMKTSTIFLVV-VLTLITGATVFKALDEOPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QMRPAGSFYATVYTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINNGIIPLGNTSSNOVSHMDGSSFFPAGVYTTIGFNGISPRTEGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTLCIGAAAFSHYEHMTFQOAYVYCTTTTIGFGDYVALOKDOALOT 216  
DB 209 ISTIFILFGCVLFALPAVIFKHEGMSALDAIFVYVITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OQOYVAFSVYILTGLTVIGAFNLV--VLREMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEVEGEFRAHAAEWMTAN 320

RESULT 5  
US-09-236-080-2  
Sequence 2, Application US/09236080

GENERAL INFORMATION:  
APPLICANT: Helen Meadows  
TITLE OF INVENTION: No. 6242217e1 Compounds  
FILE REFERENCE: GP30031  
CURRENT APPLICATION NUMBER: US/09/236,080  
CURRENT FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match 17.8%; Score 363; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 1.1e-31;  
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

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DB 42 MKMKTSTIFLVV-VLTLITGATVFKALDEOPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QMRPAGSFYATVYTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINNGIIPLGNTSSNOVSHMDGSSFFPAGVYTTIGFNGISPRTEGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTLCIGAAAFSHYEHMTFQOAYVYCTTTTIGFGDYVALOKDOALOT 216  
DB 209 ISTIFILFGCVLFALPAVIFKHEGMSALDAIFVYVITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OQOYVAFSVYILTGLTVIGAFNLV--VLREMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEVEGEFRAHAAEWMTAN 320

RESULT 6  
US-09-336-643A-83  
Sequence 83, Application US/09336643A

GENERAL INFORMATION:  
APPLICANT: Miller, Andrew P.  
APPLICANT: Curran, Mark Edward  
APPLICANT: Hu, Ping  
APPLICANT: Ruter, Marc  
TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels  
FILE REFERENCE: SEQ-15P  
CURRENT APPLICATION NUMBER: US/09/336,643A  
CURRENT FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 60/076,687  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 60/116,448  
PRIOR FILING DATE: 1999-01-19  
PRIOR APPLICATION NUMBER: PCT/US99/03826  
PRIOR FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 83  
LENGTH: 411  
TYPE: PRT  
ORGANISM: H. sapiens  
US-09-336-643A-83

Query Match 17.8%; Score 363; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 1.1e-31;  
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

OY 1 MKRONVRLALIVCFYLLVGAADFALSEPELIERORLELROOELRARNLSOGYE 60  
DB 42 MKMKTSTIFLVV-VLTLITGATVFKALDEOPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QMRPAGSFYATVYTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINNGIIPLGNTSSNOVSHMDGSSFFPAGVYTTIGFNGISPRTEGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTLCIGAAAFSHYEHMTFQOAYVYCTTTTIGFGDYVALOKDOALOT 216  
DB 209 ISTIFILFGCVLFALPAVIFKHEGMSALDAIFVYVITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OQOYVAFSVYILTGLTVIGAFNLV--VLREMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEVEGEFRAHAAEWMTAN 320

RESULT 7  
US-09-432-470-2  
Sequence 2, Application US/09432470

GENERAL INFORMATION:  
APPLICANT: David Malcolm Duckworth  
APPLICANT: Conrad Gerald Chapman  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30190  
CURRENT APPLICATION NUMBER: US/09/432,470  
CURRENT FILING DATE: 1999-11-03  
EARLIER APPLICATION NUMBER: UK 9923668.9  
EARLIER FILING DATE: 1999-10-07  
EARLIER APPLICATION NUMBER: UK 9824048.4  
EARLIER FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 393  
TYPE: PRT

ORGANISM: HOMO SAPIENS  
US-09-432-470-2

Query Match 16.1%; Score 329.5; DB 4; Length 393;  
Best Local Similarity 31.0%; Pred. No. 5.4e-28;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;

QY 9 LALIVCTFTYLLVGAANFDALSEPE-LIERORLELRODELRAKRYLSQ-----56  
DB 7 LALLALVLLVLSGALVFRLERPHQOARELGEVEREKFLRAHPVSDDELGLLKEVA 66  
QY 57 ---GGEEELERVLRKPKHAGVQMPRAGSFYFAIVYITTTIGYGHAPSTDGKVCMEY 113  
DB 67 DALGGADPEPTNSTSSSHA---WDLSAFPFSSGITTTIGYGNVALRTDARLPCIFY 123  
QY 114 ALGIPFLVMPFOSLGERINTLVRLYLLHRAKGLGMRAD-----VSANNAVLI 153  
DB 124 ALVGIPLFGILLAGVDRGLSSLRH-----GIGHLEALFLKWHVPPELVRLSAML 176  
QY 164 FFSICSTLTCIGAAAFSHYEHMFPOAYVYCFTITLTIGFGDYVALOKDQALQTOPOYVAF 223  
DB 177 LIGCLLFVLPTEFVFCYMEDMSKLEAIFYVITLTGFGDYVAGADPR--QDSPAYOPL 234  
QY 224 SEFYILTG-----LTVIGAFNLVYLRMTNNAEDKDAHRALLTRNGAGGGGG 276  
DB 235 VWFWILLGLAYFASVLTITGNMLRVYSR-----TRAEMGGLTQA 275  
QY 277 GSAHTDTASTAAG 292  
DB 276 ASWGTGTAVRTORAG 291

RESULT 8  
US-09-432-470-4  
Sequence 4, Application US/09432470  
Patent No. 6426197

GENERAL INFORMATION:  
APPLICANT: David Malcolm Duckworth  
APPLICANT: Conrad Gerald Chapman  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30190  
CURRENT APPLICATION NUMBER: US/09/432,470  
CURRENT FILING DATE: 1999-11-03  
EARLIER APPLICATION NUMBER: UK 9923668.9  
EARLIER FILING DATE: 1999-10-07  
EARLIER APPLICATION NUMBER: UK 9824048.4  
EARLIER FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 393  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-432-470-4

Query Match 16.1%; Score 329.5; DB 4; Length 393;  
Best Local Similarity 31.0%; Pred. No. 5.4e-28;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;

QY 9 LALIVCTFTYLLVGAANFDALSEPE-LIERORLELRODELRAKRYLSQ-----56  
DB 7 LALLALVLLVLSGALVFRLERPHQOARELGEVEREKFLRAHPVSDDELGLLKEVA 66  
QY 57 ---GGEEELERVLRKPKHAGVQMPRAGSFYFAIVYITTTIGYGHAPSTDGKVCMEY 113  
DB 67 DALGGADPEPTNSTSSSHA---WDLSAFPFSSGITTTIGYGNVALRTDARLPCIFY 123  
QY 114 ALGIPFLVMPFOSLGERINTLVRLYLLHRAKGLGMRAD-----VSANNAVLI 163  
DB 124 ALVGIPLFGILLAGVDRGLSSLRH-----GIGHLEALFLKWHVPPELVRLSAML 176  
QY 164 FFSICSTLTCIGAAAFSHYEHMFPOAYVYCFTITLTIGFGDYVALOKDQALQTOPOYVAF 223

DB 177 LIGCLLFVLPTEFVFCYMEDMSKLEAIFYVITLTGFGDYVAGADPR--QDSPAYOPL 234  
QY 224 SEFYILTG-----LTVIGAFNLVYLRMTNNAEDKDAHRALLTRNGAGGGGG 276  
DB 235 VWFWILLGLAYFASVLTITGNMLRVYSR-----TRAEMGGLTQA 275  
QY 277 GSAHTDTASTAAG 292  
DB 276 ASWGTGTAVRTORAG 291

RESULT 9  
US-08-749-816-2  
Sequence 2, Application US/08749816  
Patent No. 6013470

GENERAL INFORMATION:  
APPLICANT: Lesage, Florian  
APPLICANT: Gulliemare, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunki, Michel  
APPLICANT: Romey, Georges  
APPLICANT: Barhadin, Jacques  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
TITLE OF INVENTION: OF DRUGS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,816  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 989,6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-749-816-2

Query Match 15.7%; Score 320.5; DB 3; Length 336;  
Best Local Similarity 32.4%; Pred. No. 4.2e-27;  
Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9;

QY 11 LIVCTFTYLLVGAANFDALSEPE-LIERORLELRODELRAKRYLSQ-----69  
DB 26 LVIGIYLLVFGAVSVSLPEDELRLKRLKRFLEHRCLSQDLQDFLGVLA 85  
QY 70 KPHKAGV-----QMPRAGSFYFAIVYITTTIGYGHAPSTDGKVCMEY 121  
DB 86 SNVGSVLSNAGSNMMDFTSALFASVYSTGTGHTVPLSDGKGAFCIITSVIGIPT 145  
QY 122 LVMPFOSLGERINTLVRLYLLHRAKGL-----GMRADVSANNAVLI 174  
DB 146 LLEFVAVORIT-----VHVTTRPVLPHYRIRGFSKOVAVAVHALLGFLVVSCEFIP 199



REGISTRATION NUMBER: P-38,711  
REFERENCE/DOCKET NUMBER: 32,421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-332-312-4

Query Match 12.4%; Score 253; DB 1; Length 336;  
Best Local Similarity 30.3%; Pred. No. 1.3e-19;  
Matches 61; Conservative 39; Mismatches 51; Indels 50; Gaps 8;

QY 69 LKPKAGVQVRFSGSYFATVTTTGGYGAAPSTGGKFCFALGIPLLVMFOSL 128  
DB 19 VKNAATEWTWTFSSSIFFAVTVTGNGPVPVINGRIMCILFSLGIPLLVTLADL 78  
QY 129 GERI-----NTL-VRYLL--HRAK-----GLG-----MRADVSMA 157  
DB 79 AGFPLEHLWMLKNTLKLKYLKLSRKRREHVCHECHSHGMDMIEKRITAFV 138  
QY 158 NMLIGFSCISFLCIGAAAFSHYEHWTFFQAYYCFITLTTGFGDYVALQDQALQTO 217  
DB 139 LAILIYV-----TAFGVLMKLEPMSFTSFYMSFTTWTVTGFGDLP-RRD----- 185  
QY 218 PLYVAFSVYILGLVIGAF 238  
DB 186 -----GYMIIILLYITILGKF 200

## RESULT 13

US-08-332-312-2

Sequence 2, Application US/08332312  
Patent No. 5539026

GENERAL INFORMATION:  
APPLICANT: Price, Laura A.  
TITLE OF INVENTION: Functional Expression of a Drosophila  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332,312  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: P-38,711  
REFERENCE/DOCKET NUMBER: 32,421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-332-312-2

Query Match 11.3%; Score 231.5; DB 1; Length 618;  
Best Local Similarity 23.1%; Pred. No. 8.1e-17;  
Matches 94; Conservative 76; Mismatches 150; Indels 87; Gaps 16;

QY 7 RTLALVCFETVLLVGAAYFADALESEPELLERORLELROELRARNYLSGGYEEL---- 62  
DB 5 RWILLILEYISYLMFGAIIYHHHEGEKIS-----RAQORQAQAINELYLEEDKN 58  
QY 63 -----ERVVRL-----KP-----HKAGVQVRFSGSYFATVTTTGGYGAAPSTGG 106  
DB 59 TTTQDEILORISDYCKCPVTLPPYDDPTPTWTFFHAFFAFVGVSTVGGNISPPTFAG 118  
QY 107 KVCMEFYALLGIPLLVMFOSLGERINTLVRYLHRAK-----GLGMRADY 154  
DB 119 RMIMINAVSIGIVNGILFAGLGEYGRFEAYRRYKTKKSTDMHYVPQGL-----I 174  
QY 155 SMANVVLIGFSCISFL-CIGAAAFSHYEHWTFFQAYYCFITLTTGFGDYV-ALQDQ 212  
DB 175 TVVIALIPGIALFLVPCGVHLR--ELGLSSISLYSVYTTTIGFGDYVPTEGANO 232  
QY 213 ALQTOQVYAFSVYILGLVIGAFNLVYLFMTMNEDEKRDADHALLRNQAGG 272  
DB 233 KPEFGMEFYVQYLFVYVWFESLGYL--VIMTFITRGLQSKLAYLEOOL----- 281  
QY 273 GGGGSAHTTDTASSTAAGGGGFRNVYAEVLHFGQSCSLMYKREKLOYS---IPMI 329  
DB 282 -----SSNLKATQNRIMSGVTKDVGYLRLRLNL-YLVKVPYTTVDLAYTL 328  
QY 330 PDLSTSDICVEQSHSGGGGRYSDTPSR---CLCS---GAPRSA 370  
DB 329 PRNSCPDLMSYRVEPAP-----IPSRKRAFSYCADWVGAQREA 367

## RESULT 14

US-08-749-816-4

Sequence 4, Application US/08749816  
Patent No. 6013470

GENERAL INFORMATION:  
APPLICANT: Lesage, Florian  
APPLICANT: Gullenare, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunk1, Michel  
APPLICANT: Romey, Georges  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,816  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 989,6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-749-816-4

Query Match 9.3%; Score 190.5; DB 3; Length 383;  
Best Local Similarity 24.0%; Pred. No. 1.4e-12;  
Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFTYLLVGAVFDALSEPELIRORLELROQLRANV--NLQSG---GYELE-- 63  
DB 44 LVLSCTVYALGGAVLFLSIHPELKRREKAIREFODLKQOFMGNITSGIENSEQSIET 103  
QY 64 --RVLRRLK-PHKAGV-----QMRFAGSFYFAITVTITIGYHAAPSTDGK 107  
DB 104 TKKILMLLEDANHNHAEFEYFLNHEIRKDMTFSSALVFTTIVIPGYGIFFVSAYGR 163  
QY 108 VFCEFYALLGIPLTVMFQSLGERINTLVRYLLHRARKGLGMRADVSMANV----- 160  
DB 164 MCLTAVYALLGIPLTVLMADTGKFAQLV-----TRMFGDNMMAIIPAIFVCLLFAYP 216  
QY 161 -LIGFSCISITLCIGAAAFSHYEHMTFFQAVYVCFITLTITGFGDYVALQKDALQTPQ 219  
DB 217 LVVGFILCSTS-----NITYLDSYFSLTSTIFTIGFD--LTPDMNVIHMYL 261  
QY 220 VYAFSPYIILGLTVIGA 237  
DB 262 FLAVGVILVTTLDIVAA 279

RESULT 15  
US-09-144-914-7  
Sequence 7, Application US/09144914  
Patent No. 6309855  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
FILE REFERENCE: 989.6705CIP  
CURRENT APPLICATION NUMBER: US/09/144,914  
EARLIER FILING DATE: 1998-09-01  
EARLIER APPLICATION NUMBER: 08/749,816  
EARLIER FILING DATE: 1996-11-15  
EARLIER APPLICATION NUMBER: 60/095,234  
EARLIER FILING DATE: 1996-08-04  
EARLIER APPLICATION NUMBER: FR 96/01565  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 7  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog  
US-09-144-914-7

Query Match 9.3%; Score 190.5; DB 4; Length 383;  
Best Local Similarity 24.0%; Pred. No. 1.4e-12;  
Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFTYLLVGAVFDALSEPELIRORLELROQLRANV--NLQSG---GYELE-- 63  
DB 44 LVLSCTVYALGGAVLFLSIHPELKRREKAIREFODLKQOFMGNITSGIENSEQSIET 103

QY 64 --RVLRRLK-PHKAGV-----QMRFAGSFYFAITVTITIGYHAAPSTDGK 107  
DB 104 TKKILMLLEDANHNHAEFEYFLNHEIRKDMTFSSALVFTTIVIPGYGIFFVSAYGR 163  
QY 108 VFCEFYALLGIPLTVMFQSLGERINTLVRYLLHRARKGLGMRADVSMANV----- 160  
DB 164 MCLTAVYALLGIPLTVLMADTGKFAQLV-----TRMFGDNMMAIIPAIFVCLLFAYP 216  
QY 161 -LIGFSCISITLCIGAAAFSHYEHMTFFQAVYVCFITLTITGFGDYVALQKDALQTPQ 219  
DB 217 LVVGFILCSTS-----NITYLDSYFSLTSTIFTIGFD--LTPDMNVIHMYL 261  
QY 220 VYAFSPYIILGLTVIGA 237  
DB 262 FLAVGVILVTTLDIVAA 279

Search completed: July 1, 2003, 15:22:53  
Job time : 29 secs

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